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Abk87247 Bacillus
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AEB45638
AEB45612
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AEB45616
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/product= "AXMI-009"
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                                                                                                     Bacillus thuringiensis.
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-Model-frame+ p2n.model -DEV=xlh
-DB=N Geneeq -OFMT=fastap -SUFPIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=b1te -START=1 -END=-1 -MATRIX=b10eum62 -TRANS=human40.cdi -LIST-45
-DOCALIGN=200 -THR_SCORE=pct -THR_MX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNFRYT=ptc -NORM=ext -HEAPSIXE=560 -MINLEN=0 -MAXLEN=2000000000
-USER=USI0782056 @CGN 1.1.727.@runat 20012006 095214 24386 -NCPU=6 -ICPU=3
-NO WMAP -NGS SCORES=0 -WAITT -DSPBLOCK=100 -DEV TIMEOUT=120 -WARN TIMEOUT=30
-THREADS=1 -XGAPEXT=0.5 -PGAPEXT=0.5 -PGAPEXT=7 -YGAPEXT=7 -YGAPEXT=7
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Adr89409 AXMI-009
Adr89411 AXMI-009
Abk87234 Bacillus
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Biocceleration Ltd
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Copyright (c) 1993 - 2006
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ABK87234
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Gly11e1leSerArgLeu1leGly11eLeuTrpAlaGlyProAspProPheGluAlaLeu
                 CTTAGAGAGCTAGAAGGTTTACAGGGAATTATGAGACTATATCAAACTAGACTGCAAGCA
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                                                                  MetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsnAla
                                                                                                  ATGGTTCTTGTTGAAGAGCTTATTAAGAAAGTATAGATCAGCGTGTAAGAGAAAATGCT
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        20-FEB-2003; 2003US-0448633F.
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19-FEB-2004; 2004US-007812979.
19-FEB-2004; 2004US-00782020.
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sessociated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.
                                                                                                                                                                                                                                                                                                                                                New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.
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expression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
pesticidal activity.
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GGGGTCCCTTTGGCAAGTCAATCATTTGGAATAATTAGTAGGCTAATAGGTATTTTATGG
                     AlaGlyProAspProPheGluAlaLeuMetValLeuValGluGluLeuIleLy8Ly8Ser
                                     AGACTATATCAAACTAGACTGCAAGCATGGCTAGTTAACAAGAATGATGACAATCGGGAGG
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This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for associated proteins that have pesticidal activity, or for delta-endotoxin or delta-endot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.
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20-FEB-2003; 2003US-0448632P.
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20-FEB-2003; 2003US-0448907P.
20-FEB-2003; 2003US-0448910P.
20-FEB-2003; 2003US-0448910P.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782096.
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19-FEB-2004; 2004US-00782096.
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P-PSDB; ADR89412.
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Sequence 1986 BP; 659 A; 310 C; 395 G; 622 T; 0 U; 0 Other;

120 240 101 81 41 9 61 ThrasnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIle ACGAACTATAAAGAATGGCTAAATATGTGTGATTCAAATACACAATTTATTGGTGATATA AGCACGTATTCTAGCCCTGAAGCTGCTTTAAGTGTACGAGATGCTGTTTTAACGGGTATT AACAGTGTAGGGACTATACTTTTCGAATTTAGGGGTCCCTTTTGCCAAGTCAATCTTTGGA SerThrTyrSerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGly1le AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 1986 661 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: (1-1986)US-10-782-096-2 (1-682) x ADR89411 5.76e-313 3488.00 100.0% 100.0% 97.0% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: 42 61 62 121 82 181 102 ò 셤 a a a Š ઠે ò ઠે

1380 1260 1320 840 361 381 401 421 441 461 181 201 221 600 241 999 261 720 281 780 301 321 341 481 AsnalaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSer 501 AGAGAGCTAGAGGTTTACAGGGAATTATGAGACTATATCAAACTAGACTGCAGCATGG AsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAspMetThrLeu AsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluI]eLeuLeuLeu LeulleArgGluTyrLysAapHisCyslleThrPheTyrAsnGlnGlyLeuAsnGlnPhe GAAAATGGAAATGATGGTTCTGAAATAACCCATAACTTTGGTAAAACTGATTCTATTACT ArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGlnAlaTrp LeuValAsnLysAsnAspAspAsnArgArgAlaLeuValThrGlnTyrAlaIleValAsp CEGATTAGAGAATATAAAGATCATTGTATAACATTCTATAACCAGGGTTTAAATCAATTT ThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyrProLeuAla GTAAAAACGGAATTGACTAGGGAAGTTTATACAGATCCAGTAGGGTTTACTGGGGTATTA ValLeuvalGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsnAlaLeu GTTCTTGTTGAAGAGCTTATTAAGAAAGTATAGATCAGCGTGTAAGAGAAAATGCTCTT GlyalaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArgLeuGlnGly GGAGCACAGTGGCAATTAGGTGATGATGATGAATTCGTGATAATTATATCAGACTACAAGGA ACAGIATIAGAICICGCAATAITATITICCAAACIAIGAICCACGIAGGIAICCAITAGCA VallysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThrGlyValLeu GluSerGlyGlyArgThrTyrProTrpTyrAanProAsnAsnThrThrPheThrAlaMet GluAsnAsnAlaArgArgArgProSerTyrThrTrpLeuAsnArg11ePheValTyr GludanGlydandapGlySerGluIleThrHisAsnPheGlyLysThrAspSerIleThr CCTATTCAATATTTTAATTTTGCGGAACCTTTCTGTTTTCAGTATTGAGTCACTTGCTCGT IleTyrLeuGlyGlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSerArg GTTATTTTTAATACATCAAATATAAATAATGTACCTGGATCTTTAAGATACGAAGTGCCT GCTAATCTTCCATCCCAAACTATATCAGAATTACCAGGAAAGGATAAGCCAAGACA ProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIleGluSerLeuAlaArg ValllePheAsnThrSerAsnIleAsnAsnValProGlySerLeuArgTyrGluValPro AlaAsnLeuProSerGlnThrIleLeuSerGluLeuProGlyLysAspLysProArgPro 361 1021 1081 1141 122 301 421 262 781 302 901 342 961 1201 462 482 142 162 182 481 202 541 222 601 242 661 721 282 841 322 362 382 402 422 442 1261 8 6 ò 셤 ઠે 셤 ઠે 셤 ò g ઠે g ઠે 중 음 쉽 Š 셤 ò 유 ò ద ઠે a ò g 셤 유 셤 ઠે 셤 ò 8 Š ઠે

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                                                                                                                                                                                                                                                                                                          AATATCGGGTTTGTCATCCCAGGACCTACTGGGGGGAATTTGGTAAAGTCAGTGATAGT
                                                                                                                                                                                                                                                                                                                                                                                                         IleValSerPhePheAspCysSerAsnSerSerGlyArgProSerAsnThrLeuLeuGlu
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SerSerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArg
                                                                                                                           AGTTCAGGCGGTATTGTTAGTCTTTAACGTTTGGTTGGGCACATACCAGTATGGATCGT
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The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn roctworm or pouthern corn roctworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present nucleic acid sequence encodes a Bacillus thuringiensis wild-type Cryl218
                                               isolated pesticidal polypeptide useful for impacting insect pest e.g.
                                                                                                                  Page 91-96; 176pp; English
                                                                     Colorado potato beetle.
                                                                                                                                                                                                                                                                                                                                                                                                                                        endotoxin protein
                                                                                                                  Claim 1;
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0 U; 0 Other; C; 771 G; 965 T; Sequence 3621 BP; 1277 A; 608

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LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218

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1603 TTACCGTTTGTTCCAGTGGTAAAAGGACCAGGACATACAGGAGGGATTTATTACAGTAT 559 SerAspSerTrpHisSerLeuLysVal	Db 1813 ACAATGAACCCAGGTGAGGATCTGACATCTTAAAGTTGCAGATGCTATCACA 1872 Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg 644 ii iii 1873 ACATTAAATTTAGCAACAGATAGTTCGCTAGCATTGAAACATAATTTAGGTGAAGACCCT 1932 Qy 645ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn 662 1933 AATTCAACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCCCAGTAGATGAG 1992 Cy 663 ThrPheProAsnGlnSerLeuGluLysAargGluGlaGluCalagatagate 681	1993 ACTATGAAGCGGAACAAGATTTAGAAGCAGCGAAGAAAGCAGTGAATGCCTTGTTTACG 682 Asn 682	ADL15304 8t ADL15304; 06-MAY-2004	<pre>KW endotoxin; proteolytic site; insect gut; pesticidal; agriculture; KW plant pest; Cry8-like delta-endotoxin; Cry1218-1; Cry8Bb1; ds; gene. XX OS Bacillus thuringiensis. XX PN WO2004003148-A2. XX PD 08-JAN-2004. XX PF 25-JUN-2003; 2003WO-US020027.</pre>	XX XX 26-JUN-2002; 2002US-0391786P. PR 04-APR-2003; 2003US-0460787P. XX A (DUPO) DU PONT DE NEMOURS & CO E I. XX PI Abad AR, Plannagan RD, Herrmann R, Kahn TW, Lu AL, Mccutchen BF; PI Presnail JK, Wong JFH, Yu C; XX DR WPI; 2004-083033/08. DR P-PSDB; ADL15305. XX	PT New endotoxin comprising a mutation consisting of the alteration of at PT least one proteolytic site, where stability of the endotoxin in insect PT least one proteolytic site, where stability of the endotoxin in insect PT gut is increased, useful for providing improved pesticidal activity. XX XX XX The invention relates to a novel endotoxin having a mutation consisting
583 CCATTCCTTACTGTATATGCAATGGCGACCTTCATTACTGTTATTAAAGGACGCG 642 219 ASPTyrPheGlyalaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238 643 TCAATTTTCGAGAAATGGCGATGCTCAACTATTAATAACTATTATAACTATTACACTGT 702 239 LeuGlnGlyLeuIleArgGluTyrLySASpHisCysIleThrPheTyrAsnGlnGlyLeu 258 100 CAAATGAAACTTACTGGAGAATATTCTGATCACTGTGTAAAGTATTAATAACTATTATAGATCGT 702 259 AsnGlnPheAshArgSerAsnAlaGlnAspTrpValSerPheAsnArgGrTTA 762 259 AsnGlnPheAshArgSerAsnAlaGlnAspTrpValSerPheAsnArgGrTTAAB 101		339 ThralaMetGlüAsnAsnAlaArgArgProSerTyrThrThrTrpLeuAsnArg11e 358 ::: :::::		ACTCTATCAAAGGATGCAGTACTCCTTGATATTGTTTACCCTGGTTATACG	470 LeuSer	523 ABNARGLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn 542 :::

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of the alteration of at least one proteolytic site, where the stabflity of the endotoxin in an insect gut is increased relative to an endotoxin lacking the mutation. The endotoxin of the invention may be useful for providing improved pesticidal activity against insect pests whilst the compositions of the invention may be useful in agriculture for controlling pests, including plant pests. The current sequence is that the a DNA related to Bacillus thuringiensis strain 1218 Cry8-like deltaendotoxin Cry1218 of the invention.
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AGTCCAAATAATCAAAATGAATATGAAATTATAGATGCGACACCT---TCTACTTCTGTA
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AAAGCAGGAAATATCGTGTAAGACTGAGATATGCTACT------GATGCA 1767
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                        GCAAAATTAAAAGGCACGAGCGCTAAACAATGGGTTGACTATAACCAATTCCGTAGAGAA
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1993 ACATATGAAGCGGAACAAGATTTAGAAGCAGCGAAGAAAGCAGTGAATGCCTTGTTTACG 2052
                                                              1813 ACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCAGATGCTATCACA 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequence encoding a pesticidal polypeptide having an engineered protective tencoding a pesticidal polypeptide having an engineered protective the pesticidal polypeptide from proteclytic protection site, which is not sensitive to the plant protease and protects the pesticidal polypeptide from proteclytic inactivation in a plant. Also included are protecting (MI) a pesticidal polypeptide from proteclytic inactivation in a plant (comprising altering a proteclytic site within the pesticidal polypeptide that is sensitive to a plant protection site; where the protection site is not sensitive to the plant protease and protects the pesticidal polypeptide from proteclytic inactivation in a plant), an expression cassette (II) comprising the nucleic acid, a
                                      631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule having nucleotide sequence encoding pesticidal polypeptide comprising engineered proteolytic protection site resistant to protease, useful for protecting plant from pest e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to an isolated nucleic acid molecule comprising
                                    SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly
                                                                                                              1873 ACATTAAATTTAGCAACAGATAGTTCGCTAGCATTGAAACATAATTTAGGTGAAGACCCT
                                                                                                                                        ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn---
                                                                                                                                                                                              ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnValAsnAspLeuPhelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                     plant; insecticide; pesticide;
  IlePheThrProSerIleAsnProLeuIleArgTyrArg-
                                                                                                                                                                                                                                                                                                                                                                                                           B. thuringiensis Cry toxin, Cry1218-1 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis; strain 1218-1.
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DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                                                                                              AEB45606 standard; DNA; 3621
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                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                     Toxin; ds; gene; transgent plant insect pest; Cry8
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Schepers EJ, Wong JE;
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cransformed plant (III) a stably incorporated with the expression cassette in its genome, a transformed seed of the plant and an isolated pesticidal polypeptide (IV) having proteclytic activity (and comprising an engineered protection site, which is not sensitive to the plant protease and protects the pesticidal polypeptide from proteolytic inactivation in a plant). The pesticidal polypeptide is Cry8Bbi toxin or its variant or fragment, where the variant and the fragment have pesticidal activity and the variant has at least 70 % sequence identity to an amino acid sequence for the Cry8Bbi toxin. The nucleic acid and/or expression cassette are useful for protecting a plant from a pest, where expression of the nucleic acid and/or expression cassette and variant and where the produces the pesticidal polypeptide in the plant, and where the pesticidal polypeptide in the plant from the pest. The plant corporate a cysteine protease. The pest is chosen from Colorado potato beetle, Western corn roctworm, Southern corn roctworm, and boll weevil.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463 GAATGGGAAGAAATCCAAATGGTTCAAGAGCCTTACGAGATGTGCGAAATCGATTTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; 771 G; 965 T; 0 U; 0 Other;
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y d	1663	Db 1723 AAAGCAGGAAATATCGTGTAAGACTGAGATATGCTA	Qy 592 llePheValGluHisSerGlySerSerHisIleValS	Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspP :::		1873 A	Oy 645ThrGinSerPneGivTnrHisAlaileAspLyBP ::: ::: ::: ::: ::: Db 1933 AATTCAACATTATCTGGTATAGTTTACGTTGACCGAA	Qy 663 ThrPheProAenGlnSerLeuGluLyeArgGluG 	Oy 682 Asn 682	Db 2053 AAT 2055	RESULT 7 AEB34684 LD AEB34684 standard; DNA; 3621 BP. XX	AC AEB34684; xx 22_cep_2006 (figer party)	Bacillus thuringiens		OS Bacillus thuringiensis. XX PN WO2005063996-A2.	XX PD 14-JUL-2005.	XX PP 20-DEC-2004; 2004WO-US042736. XX	23-DEC-3	(DION-) PIONEER HI-BRED INT INC. (DUPO) DU PONT DE NEMOURS & CO	PI Abad A, Flannagan RD, Herrmann R, Lu A, MC PI Presnail JK, Rice JA, Wong JF, Yu C;		PT Protection of plants from insect pests comprise PT polynucleotide construct that comprises a nucl prisect protoxin; and cleavage of the protoxin print of the protoxin print protoxin p	Example	XX CC The invention relates to a method of protectin CC Dest comprising introducing a polynucleotide c CC nucleotide sequence encoding an insect protoxi CC promoter that drives expression in the plant,	
219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238	:::	239 LeuGlnGlyLeulleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258	AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp :::	763 GCAAAATTAAAAGGCACGAGCGCTAAACAATGGGTTGACTATAACCAATTCCGTAGAA 822 279 MetThrLeuthrValLeuAspLeuAlaileLeuPheProAsnTyraspProArgArgTyr 298 		299 ProbewalavallysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318 :: 883 CCANTGGAAAGGAAAGCAACTAACAAGGAAGTATACAGATCCACTGGGGGGGG	319 GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338	ArgArgProSerTyrThrThrTrpLeuAsnArgile	988 GGAGTGATAGAATCTATCGACCCCCATGTATTTGATTATATAAACGGGACTC 1047		377 GlyHisThrLeuValGluAsnGlyAsnAspGlySerGlulleThrHisAsnPheGly 395 ::: 1105 GGTCATCAAATAAGCTATCGTTGAGTAGTAGTAATCTTCAACAAATGTAGTA1164		actaatcaaaatctacacagcactagtacctttgattttacgaattatgatatttacaag	416 IleGluSer	AsnTyrileThrSerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnile		450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrile 469 1327 AhTATACAGAAAACTTAAACTTATATCCAGTTTCCAAAATATT 1374		 TACAAGAGATTCGGAATTAGAATTACCTCCAGAAACTTCAGATCAACCAAAT	483 AlaGlyAspPheserHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer 502 1435 namaagmosmanaphanaphanaphanaphanaphanaphanaphanap	TATO TATO		1546 AATACAATATATATAGATAAAATCACTCAAATTCCGGCCGTTAAATGTTGGGATAAT 1602	543 IleGlyPheValileProGlyProThrGlyGlyAsnLeuValLy9Val 558 ::: 1603 TACCGTTTCTTCCAGTGAAAGGACCAGGACATACAGGAGGGATTTATTACAGTAT 1662	
ò	g	8 8	ੇ ਨੇ 1	8 &	අ ද	සි ජ	රු පි	8	음 ;	8 8	è 8	ò	g	දි සි	ò	<u>අ</u>	දි දි	ò	g	કે ક	3 8	8 8 8	S &	පි ජි	

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|||striaaagtrgcagargcratcaca 1872
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sAAAGCAGTGAATGCCTTGTTTACG 2052
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\GCTCGATATGGCCTAGCATTAGAA 1722
                                                                                                                                ACT-----GATGCA 1767
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SAAACATAATTTAGGTGAAGACCCT 1932
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                                                                                      aCysLeuValThrHisGlyAspAla 591
                                                                                                                                                                             SerPhePheAspCysSerAsnSer 611
                                                                                                                                                                                                                                                                                                                                                      rArg----- 644
-----GlnAlaProGln 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insecticide; pesticide; ds.
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559 SerAspSerTrpHisSerLeuLysVal----
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comprise a cleavage site that is sensitive to a plant protease (within the plant), where expression of the construct produces the insect protocxin in the plant, where cleavage of the protoxin by a plant protease (within protoxin in the plant, where cleavage of the protoxin by a plant protease produces an active insect toxin and where the active insect toxin is produces an active insect toxin and where the active insect toxin is protocxin, an isolated nucleic acid molecule comprising a nucleotide sequence encoding the insect protoxin, an isolated nucleic acid molecule comprising a nucleotide sequence encoding a Cry8-like insect protoxin, impacting an insect pest of a plant comprising providing a transgenic plant that comprises in its genome a stably incorporated polynucleotide construct and a composition comprising at least one insect protoxin in combination with a carrier. The composition is useful for impacting insect pests (e.g. Colorado potato beetle, western corn rootworm, southern corn rootworm or boll weevil) on plants (e.g. monocot (maize) or dicot). The conjunction with endogenous plant or insect gut proteases) are effective in pest management strategies. This sequence represents Bacillus thuringlensis Cry8Bbl protoxin DNA of the invention. 888888888888888888888888888888888

Sequence 3621 BP; 1277 A; 608 C; 771 G; 965 T; 0 U; 0 Other;

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3621 248 219 276 25		3 SerTyrLygAgnLygAgnUTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 2:	4 AGTCCAAATAATCAAAATGAATATGAATTATAGATGGGACACCTTCTACTTCTGTA 6
Length: Matches: Conservative: Mismatches: Indels:	(1-3621)	TyrGluMetLeuAspAla	TATGAATTATAGATGCG
3.61e-77 948.00 50.98 34.48 16.48	x AEB34684	AshLysAsnGlu	AATCAAAATGAA
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	US-10-782-096-2 (1-682) x AEB34684 (1-3621)	2y 3 SerTyrLysi	ob 4 AGTCCAAAT

È	m	SerTyrLysAsnIysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
οp	4	AGTCCAAATAATCAAAATGAAATTATAGATGCGACACCTTCTACTTCTGTA 60
ò	23	SerABnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
QQ	61	TCCAATGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAAATGCGCTACAAAATATG 120
ò	43	ABBITYLLYBGluTrpLeuABBMetCysABpSerABBThrGlnPheIleGlyABpIleSer 62
ą	121	::: :::: GATTATAAAGATTATTTAAAAATGTCTGCGGGAAATGCTAGT 162
ò	63	ThrTyrSerSerProGluAlaAlaLeuSerValArgAgpAlaValLeuThrGlyIle 81
qq	163	GAATACCCTGGTTCACCTGAAGTACTTGTTAGCGGACAAGATGCACCTAAGGCCGCAATT 222
ò	82	AsmSerValGlyThrIleLeuSerAsmLeuGlyValProLeuAlaSerGlnSerPheGly 101
qq	223	::: ::: GATATAGTAGGGTCCCATTTGTTGGCCGATAGTGAGT 282
È	102	IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAspProPheGluAla 119
QQ	283	CTTTATACTCAACTTATTGATATTCTGTGGCCTTCAGGGAAAAGAGTCAATGGGAAATT 342
ò	120	LeuMetValLeuValGluGluLeulleLysLysSerIleAspGlnArgValArgGluAsn 139
Db	343	TTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATAGCAGAATATGCAAGGAATAAA 402
È	140	
οg	403	GGGCTTTCGGAATTAGAAGGATTAGGTAATAATTACCAATTATATATA
ò	160	AlaTrpLeuValAsnLysAsnAspAspAsnArgArgAlaLeuValThrGlnTyrAla 178
qq	463	GAATGGGAAGAAATCCAAATGGTTCAAGAGCCTTAGGAGATGTGCGAAATGGATTTGAA 522
È	179	IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
ор	523	
ò	199	LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218

6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8	583 239 239 239 239 239 239 239 239 239 239	
음 <i>&</i>	1495 A	accdcarragiaccrGrafifircriddacachfcgadfgcadafriadac 1545 AgnargLeuGluProagpLygileThrGlnileAspAlaValLygGlyfrpGlyGlyAgn 542
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È	543 I	IleGlyPhevalIle

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1433 CAAATGAAACTTACTGCAGAATATTCTGATCACTGTGAAAGTGGTATGAAACTGGTTTA 1492
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                                                                                           Sequence 4874 BP; 1707 A; 787
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948.00
50.9%
34.4%
                                                                                                                                                  Best Local Similarity:
                                                                          endotoxin protein
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                                                                                                                                                                                                                                                                                                                                                                                                             Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest; Colorado potato beetle; western corn rootworm; southern corn rootworm; insect target range; endotoxin; Cry1218; gene; ds.
                   -----GlnAlaProGln
                              ArgGlnThrSerTyrArg1leArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla
                                                                                          592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer
                                                                                                                               SerGlyArgProSerAsnThrieuLeuGluSerAspPheArgTyrIleAspValProGly
                                                                                                                                                                                                                                            ThrPhe----ProAsnGlnSerLeuGluLysArgGluGluValAsnAspLeuPhelle
                                                                          -----GATGCA
                                                                                                                                                                                                      ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated pesticidal polypeptide useful for impacting insect Colorado potato beetle.
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                                                                 :::
Aaagcaggaaatatcgtgtaagactgagatatgctact-----
                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis genomic Cry1218-1 DNA sequence
                                                                                                                                                                  IlePheThrProSerIleAsnProLeuIleArgTyrArg----
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                   SerAspSerTrpHisSerLeuLysVal--
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23-OCT-2001; 2001US-00032717.
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spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present nucleic acid sequence encodes a Bacillus thuringiensis wild-type Cry1218
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AGTCCAAATAATCAAAATGAAATATGAAATTATAGATGCGACACCT---TCTACTTCTGTA 790
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TCCAATGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAAATGGGCTACAAAATATG 850
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                                                                                                                                                                                                                                                                                                        Other;
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119
276
78
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Matches:
Conservative:
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Sequence 4874 BP; 1707 A; 787 C; 1003 G; 1377 T; 0 U; 0 Other;
            2498 GATATTĠTATTGĊATGTAAACGATGCTCAGATTCAG---
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JK, Wong JFH,
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                                                                                                                                                                   GGAGTGATAGAATCATCCGTTATTCGACCACCCCATGTATTTGATTATATAACGGGACTC 1777
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                                                                                                                                                                                                                                                                                                              416 IleGluSer-------LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
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                                                                            ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr
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                                                                                                                GlyvalLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe
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1835 GGTCATCAAATAAGCTACCATCGTGTCGTAGGGGTAGTAATCTTCAACAAATGTATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAgpArgAgn
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2723 ACATATGAAGCGGAACAAGATTTAGAAGCAGCGAAGAAAGCAGGGAGTGAATGCCTTGTTTAGG 2782 itiais de la composita della composita della composita della composita della c The invention relates to a novel endotoxin having a mutation consisting of the alteration of at least one proteolytic site, where the stability of the andotoxin in an insect gut is increased relative to an endotoxin lacking the mutation. The endotoxin of the invention may be useful for providing improved pesticidal activity against insect pests whilst the compositions of the invention may be useful in agriculture for controlling pests, including plant pests. The current sequence is that of the a DNA related to Bacillus thuringiensis strain 1218 Cry8-like delta-endotoxin Cry1218 of the invention. New endotoxin comprising a mutation consisting of the alteration of at least one proteolytic site, where stability of the endotoxin in insect gut is increased, useful for providing improved pesticidal activity. ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPhelle 592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 2603 ACATTAAATTTAGCAACAGATAGTTCGCTAGCATTGAAACATAAATTTAGGTGAAGACCCT ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn---SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrlleAspValProGly Mccutchen BF; endotoxin; proteolytic site; insect gut; pesticidal; agriculture; plant pest; Cry8-like delta-endotoxin; Cry1218-1; Cry8Bb1; ds. ĄĽ, 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----thuringiensis strain 1218 Cry1218-1 (Cry8Bb1) gDNA 3

319 GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338 1673 AACGTGTCTTCAATTGGTTCC	GlyHisThrLeuValGluAsnGlyAsnAspGlySerGlulleThrHisAsnPheGly :: ::: :::	431 ABITYILEThrSerGlnTyrGlyValSerArgValIlePheABIThrSerAsille 449 430	SerGlyGlyIleValSerLeuLeuThrPheGlyTrpalaHisThrSerMetAspargAsn ***:	572 ArgdinThrSerTyrargileArgleuArgTyrAlaCysLeuValThrHisGlyAspAla 591 3453 AAAGCAGGAAATHCGTGTAAGACTGAGATATGCTACT
8 6 6 6 6	8 6 8 6 6	8 6 8 6 8 6 8	3 3 <td>& & &</td>	& & & & & & & & & & & & & & & & & & &
ignment Scores: ed. No.: 5.46e-77 Length: 94874 ore: 948.00 Matches: 248 ore: 948.00 Matches: 248 ore: 948.00 Matches: 25 ery Match: 12 Gaps: 25 -10-782-096-2 (1-682) × ADL15320 (1-4874) 3 SerTyrLygAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 11 3 SerTyrLygAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 11 12 3 SerTyrLygAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 11 12 3 SerTyrLygAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 11 11 11 11 11 11 11 11 11	DD 734 AGTCCAAATGAAATGAAATTATAGATGACACCTTCTACTTCTGTA 790 QY 23 SerAsnCysTyrProArgTyrProLeualaLysAspProGlnMetThrMetArgAsnThr 42	Oy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101 553 GATATAGTAGGTAAATTACTATCAGGTTTAGGGGTCCCATTTGTTGGGCCGATAGTGGT 1012 Oy 102 IlelleSerArgLeuIleGlyIleLeuTrpAlaGlyProAspProPheGluAla 119 510 IlelleSerArgLeuValGlyIleLeuTrpAlaGlyProAspProPheGluAla 119 511 IlelleSerArgLeuValGlyIlelleUSERIIleAspGlnArgValArgGlAATT 1072 Cy 120 LeuMetValLeuValGluGluLeuIleLyBLySErIIleAspGlnArgValArgGluAsn 1139 512 IllelleValGlaGlyIleUILeuIleLyBLySErIIleAspGlnArgValArgGluAsh 1132 Cy 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159 513 GCGCTTTCGGAATTAGAAGGAATTAGGAATAATACCAATTAARCTAACTGCGCTTGAA 1192	160 AlaTrpLeuValAsnLysAsnAspAspAsnArgArgalaLeuValThrGlnTyrAla	Oy 239 LeuGlnGlyLeulleArgGluTyrLyBAspHisCysIleThrPheTyrAsnGlnGlyLeu 258

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The invention relates to an isolated mucleic acid molecule comprising a nucleotide sequence encoding a pesticidal polypeptide having an confineered protecolytic protection site, which is not sensitive to the plant protecase and protects the pesticidal polypeptide from protecolytic inactivation in a plant. Also included are protecting (MI) a pesticidal polypeptide from protecolytic inactivation in a plant (Comprising altering a protecolytic site within the pesticidal polypeptide that is sensitive to a protecolytic protection site, where the corrects the pesticidal polypeptide from protecolytic protection in a confirmation of plant protection site is not sensitive to the plant protease and protects the pesticidal polypeptide from protecolytic inactivation in a collarl, an expression cassette (II) a stably incorporated with the expression cassette in its genome, a transformed seed of the plant and an isolated pesticidal polypeptide (IV) having protecolytic activity (and comprising an engineered protecolytic protection site, which is not sensitive to the pesticidal polypeptide from protecolytic cinactivation in a plant). The pesticidal polypeptide is CryBBb1 toxin or its variant or fragment, where the variant and the fragment have controlled and activity and the variant has at least 70 % sequence identity to an amino acid sequence for the CryBBb1 toxin. The nucleic acid and/or expression cassette are useful for protecting a plant from a peet, where expression cassette in the plant
                                                                                               681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I isolated nucleic acid molecule having nucleotide sequence encoding icidal polypeptide comprising engineered proteolytic protection site stant to protease, useful for protecting plant from pest e.g.
                     ::: ||||||||||:::::
2663 AATTCAACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTAGATGAG
---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn---
                                                                     ThrPhe---ProAsnGlnSerLeuGluLysArgGluGluValAsnAspLeuPhelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice
                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic plant; insecticide; pesticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccutchen BF,
                                                                                                                                                                                                                                                                                                                                                                                    B. thuringiensis genomic DNA for Cry1218-1.
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(DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              plant insect pest; Cry8
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EJ, Wong JF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
                                                                                                                                                                                                                                                                                                                                                         892
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                                           potato
produces the pesticidal polypeptide in the plant, and where the pesticidal polypeptide protects the plant from the pest. The plant protease is a cysteine protease. The pest is chosen from Colorado potat. beetle, Western corn rootworm, Southern corn rootworm, and boll weevil. The present sequence is the genomic DNA for a wild-type Bacillus thuringiensis Cry8-like toxin.
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                                                                                                                          Sequence 4874 BP; 1707 A; 787 C; 1003 G; 1377 T; 0 U; 0 Other;
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AAT43221-T43223 represent the coding sequences for toxins that are active against scarab pests. This sequence was isolated from the Bacillus thuringiensis strain kumanotoensis. Insects in the family Scarabaeidae constitute a serious pest control problem, especially when destructive larval stage insects infest high value turf found in golf courses, playing fields and lawns. The larvae are known as white grubs, or chafer grubs, and ornamentals. The larvae are known as white grubs, or chafer grubs, and can be found in decaying organic matter, or in the soil where they consume plant roots. In Europe and the U.S. populations of these larvae and adults have developed resistance to chemical insecticides such as the organochlorines and DDT. The toxins encoded by these sequences, and intact cells that are capable of expressing the
                                                                                                                                                                                                                                                                                                                                                          2723 ACATATGAAGCGGAACAAGATTTAGAAGCAGCGAAGAAGCAGTGAATGCCTTGTTACG 2782
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                                                                                                                                                     2663 AATTCAACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTAGATGAG
                                                                                                                                                                                                                                                                                                             ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPhelle
                      SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly
                                                                                                                                                                                                                 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn---
                                                                2543 ACAATGAACCCÁGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCAGÁTGCTATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control; larval stage insect; grain; tuberous crop; white grub; chafer grub; cyclocephala; popillia; ds.
                                                                                                                632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antiscarab pest toxin 50C(b) coding sequence.
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                                                                                                                                           ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
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 many pests of the family scarabasidae, and Popillia. The toxins are active and against adults. (Updated on 16-OCT-
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AGTCCAAATAATCAAAATGAATATGAAATTATAGATGGGGACACCT---TCTACATCTGTA
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                                                             Sequence 3507 BP; 1256 A; 576 C; 732 G; 943 T; 0 U; 0 Other;
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proteins, can be used to control such as species of Cyclocephala, against larvae (present in soil) 2003 to standardise OS field)
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GAATATCCAAGAGTCATT-----TCAGTAAATGCTTCTTCAAACATACAGAGGTTATCT
                                                                                                                                                                                                                                   AspValProGlyIlePheThrProSerIleAsnProLeuIleArgTyrArgThrGlnSer
                                                                                                                                   PheGlyThrHisAla------IleAspLysPheGluPheIleProLeu
                                                                                                                                                                        1912 ATAGGTATACAAACGAATACAAATTTATTTTTAGACCGAATCGAATTCATCCAGTA
                                                                                                                                                                                                               Asn---ThrPheProAsnGlnSer---LeuGluLysArgGluGlnGluValAsnAspLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding Bacillus thuringiensis insecticidal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insecticide; transgenic; Coleoptera larvae; ss; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product= "Insecticide protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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2158 GATAAGTTCGAACTTATTCCGGTAAATGCAACATTTGAAGCAGAAGAACCTAGATGG 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present nucleic acid sequence encodes a Bacillus thuringiensis wild-type Cry1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated pesticidal polypeptide useful for impacting insect pest e.g.
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                                                                                                                                                                                                                                                                                                             Pesticidal, spraying, dusting; broadcasting; seed coating; insect pest; Colorado potato beetle; western corn rootworm; southern corn rootworm; insect target range; endotoxin; Cry1218; gene; ds.
                AsplysPheGluPheIleProLeuAsn---ThrPhe---ProAsnGlnSerLeuGluLys
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                                                                                                                                                                                                                                                                               Bacillus thuringiensis Cry1218-1 truncated gene sequence.
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23-OCT-2001; 2001US-00032717.
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1066 CCAATCGAAACAACGCCCCAACTTACACGGAAGTGTATACAGATCCAATAGTATTTAAC 1125
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                                                                                                                                                               PheValTyrThrArgThrLeuGly-----AsnMetSerAspValArgAsnIleTrp 375
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                                319 GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe
                                                       525 LeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrp-----GlyGly
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4 AGTCCAAATAATCAAAATGAAATTATAGATGCGACACCTTCTACTTCTGTA 60 23 SERABNCYSTYPFOAZGTYPPOLEUAlaLYSASPPROGINMETTHYMELAZGABNThr 42		102 IlelleSerArgLeulleGlyIleLeuTrpAlaGlyProAspProPheGluAla 119 ::: ::::	AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln	463 GAATGGGAAGAAAAATCCAAATGGTTCAAGAGCCTTACGAGATGTGCGAAATCGATTTGAA 522 179 IleValAspAsnPhePheGlubysAsnMetProLysPheLysGluArgAsnPheGluIle 198	CCATTCCTTACTGTATATGCAATGGCAGCCAACCTTCATTACTGTATTAAAGGAGGGGGABTYTPHGGTAATGCAATGGCAGCCGACCTTCATTACTGTTATTAAAGGAGGGGGGGG	239 LeuGlnGlyLeulleArgGluTyrLy8A8pHisCysIleThrPheTyrAsnGlnGlyLeu 258	279 MetThrLeuThrValleuAspLeuAlaileLeuPheProAsnTyrAspProArgArgTyr 298	GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe
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ABGIYSerGlulleThrHi8A8nPheGly 395
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TTGATTTTACGAATTATGATATTTACAAG 1224
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TACCICCAGAACTICAGAICAACCAAAT 1434
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TCACAAGTATTCCCGCGACGGGTAACACT 1494
                                                      heAsnPheAlaAsnLeuSerValPheSer 415
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---TITGGAATGCCAGAAGTCGAGTTTTTCATGGTAAACCAATTG 1326
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                                                                                                    LeuMetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
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                                                                                                                                          343 TTTATGGAACAAGTAGAAGAACTCATTAATCAAAAAATAGCAGAATATGCAAGGAATAAA
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                                                                                                                                                                                  AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by applying, dusting, broadcasting, or seed coating, where the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn roctworm or southern corn roctworm or southern corn roctworm or producing transge and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also to produce the pesticidal polypeptide of the invention is also to produce the pesticidal polypeptide of the invention. The present nucleic acid sequence encodes a Bacillus thuringiensis wild-type Cry1218
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                                          pest;
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AGTCCAAATAATCAAAATGAATATGAAATTATAGATGCGACACCT---TCTACTTCTGTA
                                     Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest Colorado potato beetle; western corn rootworm; southern corn rootworm; insect target range; endotoxin; Cry1218; gene; ds.
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Bacillus thuringiensis Cry1218-1A truncated gene sequence.
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                                                                                                                     Bacillus thuringiensis.
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P-PSDB; AAU99262.
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|AATACAATATATTCCAGATAAAATCACTCAAATTCCGGCCGTTAAATGTTGG---GATAAT 1602
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ACAATGAACCCAGGTGAGGATCTGACATCTATAAAGTTGCAGATGCTATCACA 1872
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375 ATAGCGAGTACAAGAGATTCGGAATTAGAATTACCTCCAGAAACTTCAGATCAACCAAAT 1434
                                                                                                                                                                                                                                                                                                     ------GATGCA 1767
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                                                                                                                                                            ABRARGLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn 542
                                                                                                                                                                                                  543 IleGlyPheValIle------ProGlyProThrGlyGlyAsnLeuValLysVal 558
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                                                                                                                                                                                                                                          -----GlnAlaProGln 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest; Colorado potato beetle; western corn rootworm; southern corn rootworm; insect target range; endotoxin; maize; Cry1218; gene; ds.
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AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle
                                                                             AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer
                                       ----GluLeuProGlyLysAspLysProArgProAsn
                                                                                                                     SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn
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Aaagcagggaaatatcgtgtaagactgagatatgctact----
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TCCAACGACTCCAACGCTACCCCTTCGCCAACGAGCCCACCAACGACGCCTCCAGAACATG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn roctworm or southern corn roctworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present nucleic acid sequence encodes a Bacillus thuringiensis wild-type Cryl18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleIleSerArgLeuileGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
                                                                                                                                                                                                                                                                                                                                                               New isolated pesticidal polypeptide useful for impacting insect pest e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 gagracecegerececedes de serecererentes de conserventes de conserventes estas de conserventes en conserventes estas de conserventes en cons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 114-116; 176pp; English.
(DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                        Abad AR,
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Trcatggagcaggaggaggagcrcarcaaccagaagarcgccgagracgcccgcaacaag 402 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159 AlaTrpLeuValAsnLysAsnAspAspAsnArg----ArgAlaLeuValThrGlnTyrAla 178

GCCCTCTCCCGAGCTGGAGGCCTCGGCAACAACTACCAGCTCTACCTCACCGCCCTGGAG 462

140

403 160

QQ	463 GAG	GAGTGGGAGGAACCCCCAACGGCTCCCGGGCCCTCCGCGACGTGCGCAACCGCTTCGAG 522
È	179 Ile	IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGlulle 198
οp	523 ATC	CTCGACTCCCTCTTCACCCGGTACATGCCCTCCTTCCGGTGACCAACTTCGAGGTG 582
ćo	199 Leu	LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
qq	583 CCC	TTCCTCACCGTGTACGCCCATGGCCGCCAACCTCCACCTCCTCCTCAAGGACGCC 642
ò	219 Asp	AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGlulleArgAspAspAspAspTyrIleArg 238
дg	643 TCC	ATCTTCGGCGAGGAGGGGGCTGGTCCACCACCATCAACAACTACTACGACCGC 702
ò	239 Leu	LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
qq	703 CAG	ATGAAGCTCACCGCCGAGTACTCCGACCACTGCGTGAAGTGGTATGAGACCGGCCTC 762
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Db	763 GCC	AGCTCAAGGGCACCTCCGCCAAGCAGTGGGTGGACTACAACCAGTTCCGCCGCGGG 822
È	279 Met	MetThrLeuThrValLeuAspLeuAlalleLeuPheProAsnTyrAspProArgArgTyr 298
Ωp	823 ATG	accercaccáracrica de grases de centrales de contra de co
È	299 Pro	ProLeuAlaVallysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
qq	883 CCC	ATGGAGACCAAGGCCCAGCTCACCCGCGAGGTGTACACCGACCCGCTCGGCGCCGTG 942
ò	319 Gly	GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338
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à	339 Thr	AlaMetGluAsnAsnAshAshAsqArgProSerTyrThrThrTrpLeuAsnArg1le 358
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à	359 Phe	ValTyrThrArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
qq	1048 ACC	ACCTGTACACCCAGTCCCGCTCCATCTCCCCCCCGCTACATCCGCCACTGGGCC 1104
ò	377 618	HigThrLeu: ValGluAenGlyAenAspGlySerGluIleThrHisAsnPheGly 395
qq	1105 GGC	::: GCCACCAGATCTCCTACCACCGCGTCCAGCTCCAGCAGATGTACGGC 1164
ò	396 LyB	ThraspserileThrProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
QQ	1165 ACC	ACCAACCAGAACCTCCACCTCCACCTTCGACTTCACCAACTACGACATCTACAAG 1224
ò	416 Ile	GluSer
QQ	1225 ACC	ACCTCTCTCAAGGACGCCGTGCTCCTCGACATCGTGTACCCCGGCTACACC 1275
ờ	431 Asn'	AsnTyrIleThrSerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnIle 449
Db	1276	 TACATCTTC÷TTCGGCATGCCGGAGGTGGAGTTCTTCATGGTGAACCAGCTC 1326
ò	450 Asn	AsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThr1le 469
Ob	1327 AAC	::: ::: CAAGACCCTCAAATACAACCCCGTGTCCAAGGACATC
à	470 Leu	LeuSerGluLeuProGlyLy8AspLysProArgProAss 482
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qq	1435 TAC	GAGTCCTACTCCCACCGCTCTGCCACATCACCTCCATCCCCGCCACGGCAACACC 1494
ò	503 Ser	SerGlyGlylleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn 522
DP	1495 ACC	sacercerecce ererrereridakecekecerereakeereka 1545

::: |||| | ||| 1813 ACCATGAACCCCGGCGAGGACCTCCAAGACCTTCAAGGTGGCCGACGCCATCACC 1872 1873 ACCCTCAACCTCGCACCGACTCCTCCCTCAAGCACAACCTCGGCGAGGACCCC 1932 592 IlePhevalGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611 559 SerAspSerTrpHisSerLeuLysVal-------GlnAlaProGln 571 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg------- 644 6 8 6 8 6 8 6 g ઠે q ઠે a ઠે

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DN65802 CEC32-C02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases I to 2006)
Chen, B.S., Li, Y.Z., Peng, Y.L., Dong, H.T. and Li, D.B.
Direct Submission
Submitted (108-DEC-2004) Guangxi University, Daxue Road 100,
Nanning, Guangxi 530004, China
Location/Qualifiers
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-Q=/cgn2_1/USPTO_spool/USi0782096/runat_20012006_095215_24405/app_query.fasta_1.839
-USB=EST -OFMT=fastap -SUPFTX=p2n.rst -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=b1ts -START=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST=45
-UNITS=b1ts -START=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST=45
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-USFR=USI0782096 @CGN 1_1.5315_@runat_20012006_095215_24405 -NCPU=6 -ICPU=3
-NO PMAP -NGS SCORRAS=0 -WALT -DSPBLOCK=100 -DEV_TIMEOUT=120 -WARN TIMEOUT=30
-THREADS=1 -XGAPCP=10 -XGAPEXT=0.5 -FGAPDEXT=7 -YGAPCP=10
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KANSVMKERERTRINPGYSAFWRKVLIKPTLSNOGDIBAGVTISFDGYGYBDBETFPN
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96 AlaSerGinSerPheGlylleileSerArgLeulleGlylleLeuTrpAlaGlyProAsp 115 9073 GTCAATGTAGCTCTGGATATTAAGTCGCATTCATACTATT	9220 GAAGTTATTGAATCTACAAATTTAAAATACTTC	PhelysGlubrgAsnPheGlulleLeuLeuProValTyralsGlnalaalaAsnLeu :::	231 GlulleArgAspAsnTyrIleArgLeuGlnGlyLeullaArgGluTyrLysAspHis 249 11: 1: 1: 1: 1 1: 1 1 1: 1 1 1 1 1 1 1 1 1 1 1 1 1		280 ThrLeuThrValLeuAspLeuAlaileLeuPheProAsnTyrAspProArgArgTyrPro 299	320 ValleuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThr 337 :::::		366	385AsnAapGlySerGlulleThrHisAsnPheGly 395 :::
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Z . X			. w	urce ne	/locus_tag="HC19616" Scores: 2.29 Length: 117.50 Matches: milarity: 34.4% Conservative:	Best Local Similarity: 20.2\$ Mismatches: 314 Query Match: 3.3\$ Indels: 197 DB: 11 Gaps: 38 US-10-782-096-2 (1-682) x DQ051595 (1-11493) Qy 2 AşinSerTyrLysAşanQluTyrGluMeţLeuAspAlaLeuArglleAsnSerAsn 21	8815 AACCTGGGAAGGAACAACAGCTGCACGACGTGGTGGTGGTGGAGGAGCAGGAGGAGC 8874 22 MetSerAsnCysTyrProArgTyrProLeuAlaLysAspProGln 36 8875GACTGCCCATGTGTGTGAGAGCACTTGTCCCACTGGAGCAGC 8916	37MetThrMetArgAsnThrAsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThr 55 8917 ATCTTCATGTGGAGGCAGCATCATTACCAGGCGATTGTAACTGCCTATGAGAATAGCTT 8976 56 GlnPheIleGlyAspIleSerThrTyrSerSerProGluAlaAlaLeuSerValArgAsp 75 6777 CAGCARGARCCCTATGAACGTTCATA	AlaValLeuThrGly11eAsnSerValGlyThr11eLeuSerAsnLeuGlyValProLeu
RESULT 2 DQ051595 LOCOS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL	COMMENT	08 69 196	ORIGIN Alignment Pred. No.: Score: Percent Si	Best Local S Query Match: DB: US-10-782-09 Qy	a & a	è 8 è 6	l & a

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441 ArgValIlePheAsnThrSerAsnIleAsnAsnValProGlySerLeuArgTyrGluVal 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 ProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIleGlu---SerLeuAla 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       559 GATGTGCTGAATATGGCGGCCGCACAACGGCTGGTÁTTTGATGCAGAÁCTGGACACCGTG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P. pacificus
                                                                                    1 (bases 1 to 782)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
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                         Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                      Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601371
Fax: 00497071601494
Fax: 01497071601499
Fax: 0149707
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/clone_lib="Mixed stage fosmid library ovar. California"
/note="Vector: pEpifos-5 Fosmid vector"
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Matches:
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/mol_type="genomic DNA"
/strain="California"
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   Pristionchus pacificus
                                                                                                                                                                                     Pristionchus pacificus
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117.00
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DB:
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      ORGANISM
                                                                                       REFERENCE
AUTHORS
TITLE
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PUBMED
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10237 AAAAAGTGGATCAAAATCTTGGAGGCCAAGACCAAGCAACTCCCCCAAATTCTTCCTCATA 10296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10353 -------TCCTGGGGAGTTTCTGATGCCAAAGCCAACGCATTATTACAT 10394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10455 GCGGCTGTACATCCGGGG------10484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10485 GATCTACCCATACCTCGTCATGAACGACGCCTGCCTCACAGAGTCACGGCGAGAGGAGGCG 10544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10665 GGAGGACAACCCCTCTTCACTTTCCCTTGTGGAGATCTACAAGCAGCGCTGCGCCAAGAA 10724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       638 ------ArghroLeulleArgTyr-----ArgThrGldSe 647
                                                                                              -----SerIleGluSerLeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsnAsn 431
                                                                                                                                                                                                                  432 TyrlleThrSerGlnTyrGlyValSerArgValIle-----PheAsnThrSerAsn 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnThrIleLeuSerGluLeuProGlyLysAspLysProArgProAsnAlaGlyAspPhe 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 ValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsnAsnArgLeuGlu 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 GlyPheVallleProGlyProThrGlyGlyAsnLeuValLysValSerAspSerTrpHis 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564 SerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAla 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 SerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSerGlyGlyIle
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                                                                                                                                                                                                                                                                                                                                         449 IleAsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uGluSerAspPheArgTyrlleAspValProGlyIlePheThrProSerIle-----
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                                                                                                                                   10090 TCCAGCGCAGCCTCTGAGTCTCTGGCCCGG-
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GSS.
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US-10-782-096-2 (1-682) x CL964901 (1-2982)	Oy 43 ASHTyrLygGluTrpLeuhsnMetCygAspSerAshThrGlnPheileGlyAspileSer 62	Oy 63 ThrTyrserSerProGluhlaAlaLeuSerValArgAspAlaValLeuThrGly1leAsn 82	Qy 83 SerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101	Oy 102 IlelleSerArgLeulleGlyIleLeuTrpAlaGlyProAspProPheGluAlaLeu 120	Oy 121 MetValLeuValGluGluLeuIleLy8Ly8SerIleAspGlnArgValArgGluAsnAla 140 :::::: Db 595 TCGCTCACATATGTTGACCTTGGAAACGACTCTCACAGGGGAGAATCCCAGAGTCCTTG 654	141 LeuargGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrargLeuGlnAla ::: 655 GTAAATAGTTCATCTCTACAAGTGCTTAGGCTCATGAGAATGCCCTTAGCGGA	Qy 161 TrpLeuValAsnLysAsnAspAspAsnArgArgAlaLeuValThrGlnTyrAlaIleVal 180	Oy 181 AspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeu 200	Qy' 201 LeubroValTyrAlaGlnAlaAlaAsnLeuHisLeulleLeuLeuArgAspAlaAspTyr 220	Qy 221 PheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArgLeuGln 240	241GlyLeulleArgGluTyrLysAspHisCyslleThrPheTyrAsn	256 GlnGlyLeuAanGlnPheAanArgSerAanAlaGlnAapTrpValSerPheAanArgPhe	Db 967 ATATCCTTGAATAGCAACAATCTG	066 066 qg	Cy 296 ArgArgTyrProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProVal 315	066	Oy 316 GlyPheThrGlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsn 335 Db 991TCAGGGTCAGTACCCCAATCTCTTCTAACATGTCTCTT 1029		Db 1030 creacatricerreceardataacraatracerearregaaaaarrecerreaacareege 1089	Oy 354 TrpLeuAgnArgllePheValTyrThrArgThrLeuGlyA8nMet 368 :::	Qy 369 SerAspValArgAsnIleTrpGlyGlyHisThrLeuValGluAsnGlyAsnAspGlySer 388
Cy 520AspArgAsnAsnGLeuGluProAspLysIleThrGlnIleAspAlaValLysGly 538	539 TrpGlyGanlleGlyPheVallleProGlyProThrGlyGlyAsnLeuValLygVal	559 SerAspSerTrpHisSerLeuLysValGlnAlaProGlnArgGlnT	579 ArgLeuArgTyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHisSerGly	599 SerSerHislleValSerPhePheAspCysSerAsnSerSerGlyArgProSerAsnThr		ProLeulleArgTyr 643 ::: ::: CCTATCTGGCCTTT 38	RESULT 4 CL964901 LOCUS CL964901 2982 bp DNA linear GSS 21-8EP-2004	DEFINITION OSIFCC011268 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. ACCESSION CL964901	_	Entratophyta; Magnolophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. REFERENCE 1 (bases 1 to 2982)	AUTHORS Ma,L., Wangc,j., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,W., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J. TITLE An analysis of transcriptional reculation of the rice genome and	its comparison to Arabidopsis AL Unpublished (2004) Contact: Chen Chen	Department of Bioinformatic Beijing Institute of Genomics Chinese Academy of Sciences, Beijing 101300, China	Te1: 86-10-80481559 Fax: 86-10-80488676 Fmail: chanchaimgrannming our on	Emmar: Creminghayemonire.org.cm Rice ganomic sequence. Class: exon-trapped.		sm="Oryza sativa (indica op="genomic DNA" f="taxon:39946"	/clone lib="Oryza sativa Express Library" /note≒"Oryza sativa exon trapped genomic sequences " ORIGIN	ent Scores:	0.839 Length: 113.00 Matches: ty: 32:2% Conservative:	

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Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Chrysomeloidea; Chrysomelidae; Chrysomelinae; Timarchini; Timarcha. Labaee 1 to 1298; Gomez-Zurita,7.; Kopliku,F., Theodorides,K. and Vogler,A.P. Resources for a phylogenomic approach in leaf beetle (Coleoptera)
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                                                                                                     (in) Jolivet, P., Santiago-Blay, J.A. and Schmitt, M. (Eds.); NEW DEVELOPMENTS IN THE BIOLOGY OF CHRYSOMELIDAE, 19-35 (2004) Contact: Gomez-Zurita J Department of Entomology The Natural History Wassum Cromwell Road, London SW7 SBD, United Kingdom.
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/clone_lib="1A1"
/note="country: Spain:Balearic Islands, Mallorca,
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1351 AACAATATCCAAGGGAACCTGCCAAGTACTATTGGAAATCTTTCTAGTGATCTACAGTGG 1410
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1468 AAGGGCCTCACTAAGTTGTACATGGATTACAATCTTTTGACTGGAATATACCACCAACA 1527
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Wong,G.K.S., Deng,X.W. and Wang,J. TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis JOURNAL Unpublished (2004) COMMENT Contact: Chen Chen Department of Bioinformatic Beijing Institute of Genomics Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-80488559 Fax: 86-10-8048876 Email: chenchen@genomics.org.cn Rice genomic sequence.	Class: exon-trapped. FEATURES Location/Qualifiers 12439 forganism="Oryza sativa (indica cultivar-group)" /mol_type="genomic DNA" /db_xref="taxon:39946" /clone_lib="Oryza sativa Express Library" /note="Oryza sativa exon trannod renomic semiences"	2439 3: 2439 Aktive: 108 255 246 36	3 SerTyrLygAgnLygAgnGluTyrGluMetLeuAgpAlaLeuArglle	496 AACCITCGGICAGGAIATTITCATCCGGGGAATATCIATACCATGACGAATCAGGGC 36 GlnMetThrMetArgAanThrAanTyrLyaGluTrpLeudanMetCyaAapSerAanThr 1::	604 GANTICACCATICGGAAACATCAATAATTACTGGAACTTTCTCTATTCGGAAGGGGCTC 63ThrTyrSerSerProGluala	QY 85 GlyThrIleLeuSerAshLeuGlyValProLeuAlaSerGlnSerPheGlyIleIleSer 104	124 IGluGluLeuIleLysLysSerIleAspGlnArgYslArgGluAsnAlaLeuArg 124 IGluGluLeuIleLysLysSerIleAspGlnArgYslArgGluAsnAlaLeuArg 135 III
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	224 nTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArgLeu		419 uAlaArgileTyrLeuGlyGlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyVa 439
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Qy 517 ThrSerMetAspArgAsnAsn	Qy 564 SerLeuLyBValGlnAlaPro	RESULT 10 BH770523/c LOCUS BH770523 BH770523 LOCUS DEFINITION LLMGtag287 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, genomic survey sequence. ACCESSION BH770523.1 GI:20373480	L RB R	Generique microbienne INRA CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France Tel: 33 1 34 65 25 16 Fax: 33 1 34 65 25 16 Email: sorokine@jouy.inra.fr best homologue in strain IL1403 is arcD1 (94%) Class: shotgun High quality sequence start: 30 High quality sequence start: 1898. FEATURES Location/Qualifiers	source 11926 /organism="Lactococcus lactis subsp. cremoris" /mol type="genomic DNA" /strain="MG1363" /sub_species="cremoris" /db xref="Fexaon:1359" /clone_lb="MG1363 Random Sequence Tag Library" /note="Vector: pSGMU2; Site 1: Sma1; Library of chromosomal fragments of L.Tactis strain MG1363 was prepared by partial Alul digestion or by sonication."	Alignment Scores: Alignment Scores: Pred. No.: 107.50 Matches: Score: Score: Percent Similarity: 36.4* Conservative: 40 Best Local Similarity: 21.6* Mismatches: 94 Query Match: 9 Mismatches: 97 Gaps: 10 DB: 0S-10-782-096-2 (1-682) x BH770523 (1-1926) Qy 375 TrpGlyGlyHisThrLeuValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPhe 394
ORIGIN Alignment Scores: Alignment Scores: Pred. No.: Score: 1.11 Length: 1437 Score: Percent Similarity: 34.9\$ Conservative: 55 Best Local Similarity: 20.5\$ Mismatches: 89 Query Match: 10 Gaps: 20	YThraspProvalGlyPhe :: TCAAGGATGCCATCGCGAC roTrpTyrasnProAsnAsn CT::	342 GluAsnasnalaargargargaroserTyrThrTrpLeuasnarglle	379 ThrieuvalgludenglyaenaspglyserglullethrHisaenPheglyLysThrasp 179 ThrieuvalgludenglyaenaspglyserglullethrHisaenPheglyLysThrasp 11	0.00 0.00	TTGGACCTG ABNILe TCTCTTCGA ASTYrGlu	Db 697 CCGTCAAACATTGGCTATCTCCAATGGCTCTTATTGGGTGATAACATG 756 Qy 462AlaAsnLeuProScrGlnThrIleLeuSerGluLeuProGlyLysAspLysPro 479

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/db_xref="taxon:3879"
/tissue_type="Glandular trichomes isolated from stem"
/tissue_type="Glandular trichomes isolated from stem"
/dev_atage="Trichomes were removed from internodes of 8-12
inch tall stems"
/clone_lib="Glandular trichomes"
/clone_lib="Glandular trichomes"
/note="vector: pDNR_LiB: Glandular-haired alfalfa plants
were established in a Conviron growth chamber (16-h days,
full lights, 24oC set point) in 40 one gallon pots. Plants
were grown in Metronix 350 and fertilized with MiracleGro
as needed. They were cut back closely to encourage the
emergence of vigorous shoots. Trichomes were isolated from
stems, approximately 8-12 inchemes lost clipped from plants
2-3 inches above the crown. With minimal handling of the
stem, the apical bud, leaves and nodes were discarded, and
the trichomes isolated from the internode segments."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetGluAsnAsnAlaArgArgArgProSerTyrThrThrTrpLeuAsnArgIlePheVal 360
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Eax; 580 224 6650
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TCTAAATCTTCCAAGAAGAATTCAAACCCTAATA----
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                         organism="Medicago sativa"
                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:3879"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-782-096-2 (1-682) x CO516871 (1-500)
                                                                                               Email: gdmay@noble.org.
Location/Qualifiers
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107.00
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EST 15-JUL-2004 CO516871.1 GI:50321745
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Medicago sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rogids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                        414
                                                                                                 SerileGluSerLeuAlaArgileTyrLeuGlyGlyThrGluAlaAsnAsnTyrileThr 434
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Aziz,N., May,G.D., Paiva,N.L. and Dixon,R.A.
Alfalfa trichome Expressed Sequence Tags from the Samuel Roberts
Noble Foundation - Center for Medicago Genomics Research
Unpublished (2004)
Contact: May GD
                                                                                                                                         ------GTCTTT
                                            ----TCACTTCTTGAAGCTTGGTTGTCATGGACAATGCTTCCTGTTGAAGCAACAAA
                    GlyLysThrAspSerlleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPhe
                                                                                                                                                                           SerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnIleAsnAsnValProGly
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AUTHORS
TITLE
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Klausnert, R.L., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zoeberg, B., Buetow, K.H., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Biatchenko, L., Marnsina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanius, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R. W., Bouffard, G. G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, B., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McClowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                      HTC 19-NOV-2003
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Series: IRAK Plate: 65 Row: n Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 27369963
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Straubberg, R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbe.r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                 BC032293 4979 bp mRNA linear HTC 19
Mus musculus RIKEN CDNA D030051N19 gene, mRNA (CDNA clone
LWAGE:5400613), with apparent retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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                                                                                                                                                                                                         (house mouse)
                                                                                                                                                           BC032293.1 GI:22749640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaithersburg, Maryland;
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                                                                                                                                                                                                                                       Mus musculus
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KEYWORDS
SOURCE
ORGANISM
                                                                            DEFINITION
RESULT 12
BC032293
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AUTHORS
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AUTHORS
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JOURNAL
                                                                                                                                ACCESSION
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COMMENT
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Location/Qualifiers 1. .4979 /organism="Mus musculus"

FEATURES

/mol_type="mRNA"

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996 CCTCTCCTCCACAATTTCCTGCACATGCTGTCCTCCCGTTCCTCTGGCATCCAGACCGAG 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1512 CAATGTGACCTGAGACGCTTCTTTTGGAGTATGACAGGCTGCAGGAGGTGGATCAGAGC 1571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 ArglleTyrLeuGlyGlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSer 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          936 ACAGAGITATCTCATTACCGTCAACGTGCCCTCCTGCAATCACAGCCAGTTCGCCGGACA 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                            304 ThrGluLeuThrArgGlu-------ValTyrThrAspProValGlyPheThr 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 ProSer -- TyrThrThrTrpLeuAsnArgIlePheValTyrThrArgThrLeuGlyAsn 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1278 ACAGTACTCACTCTGAACTCTCTGAGGTAGAATCTATGCCCCCACCGAGG---ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1395 TCTGTGTATACTTCAGCCACAGAGGGAGGGGTTTTCCATCATCAGGGTTGGCAACTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 ProTrpTyrAsnProAsnAsnThrThrPheThrAlaMetGluAsnAsnAlaArgArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HisThrLeuValGluAsnGlyAsnAspGlySerGluIleThr---
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                                                                                                                                                                                                                       4979
84
51
111
119
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Mismatches:
Indels:
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                                                                                                                       /note="Vector: pCMV-SPORT6"
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578 leargLeuArgTyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHisSerG 598
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CGTCCACTGTGATGCCAGACCCAGTGGTGAAGCCAGCACAGTACCAGAAGTGGCCCGGT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 lyAsnIleGlyPheVallleProGly------ProThrGlyGlyAsnLeuValLy8V 558
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                                  ValLeuAspLeuAlaIleLeu---PheProAsnTyrAspProArgArgTyrProLeuAla 301
                                                                                                   ValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThrGlyValLeu 321
                                                                                                                                                                        GluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPheThrAlaMet 341
                                                                                                                                                                                                         GAGACGGCGATTCGCGCACTCCGATGAGACGCCGGAGCACTCGGATC-----123
                                                                                                                                                                                                                                         GluasnasnalaargargargProSerTyrThrThrTrpLeuAsnarg1lePheValTyr 361
                                                                                                                                                                                                                                                                   ThrargThrLeuGlyAsnMetSerAspValargAsnIleTrpGlyGlyHisThrLeuVal 381
                                                                                                                                                                                                                                                                                                                                                                                 GluAsnGlyAsnAspGlySerGluIleThr-HisAsnPheGlyLysThrAspSerIleTh 401
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|CTCAACCCTGGCTCCGGGTCTAACAGCCCCTGGCAAAAGGAAGCAGAAACTGAGATTAT
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GTAGGAGTGCTGATGTCTCATCCTTGGCTAGC------
                                                                                                                                        GTACGCACGCTTTTGCGGCGC-------
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US-10-782-096-2 (1-682) x BI079460 (1-981)
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                               1785 TACTCATCTGGT------GAGGCTAGCTCTTCCTGGCACGTCTCCACTACCTTTGAG 1835
                                -----AACAATGATACCCTTCGTTGGGAAAGA 1772
                                                                                                                                                                                                                                BI079460 981 bp mRNA linear EST 20-JUN-2001 602873864F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5005694 5',
                                                                                                     ------CCTAAC 1784
                                                                                                                                        550 ProThrGlyGlyAsnLeuValLysValSerAspSerTrpHis---Ser-LeuLysValGl 568
                                                                                                                                                                                                            nAla---ProGlnArgGlnThrSerTyrArgIle-----ArgleuArgTyrAlaCysle 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contect: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11045 row: p column: 15
High quality sequence stop: 764.
Location/Qualifiers
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
LeuThrPheGlyTrpAlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspLys
                                                                 530 IleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsnIleGlyPheValIleProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 981)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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144
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Unpublished (2004)
Contact: Chen Chen
Department of Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80488576
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: con-trapped.
Location/Qualifiers
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AlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThrGlyVal 320
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APPLICANT: Michaels, Tracy Ellis
APPLICANT: Michaels, Luis
APPLICANT: Foncertada, Luis
APPLICANT: Proncertada, Luis
APPLICANT: Proncertada, Luis
APPLICANT: Proncertada, Luis
TITLE OF INVENTION: Process for Controlling Scarab Pests
TITLE OF INVENTION: with Bacillus thuringlensis Isolates
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Sulte A-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
US-08-961-803-5

US-09-661-322A-62

US-09-661-322A-62

US-09-178-252-22

US-09-178-252-22

US-08-459-448A-6

US-08-459-595A-6

US-08-459-595A-6

US-08-459-595A-6

US-08-459-595A-6

US-08-459-595A-6

US-08-459-595A-6

US-08-459-595A-6

US-09-661-322A-41

US-09-988-462-6

US-09-988-462-6

US-09-988-462-6

US-09-988-462-6

US-09-988-462-6

US-09-961-322A-41

US-08-176-865-3

US-08-176-865-3

US-08-176-865-3

US-08-176-865-3

US-08-176-865-3

US-08-176-865-3

US-08-176-865-3

US-08-991-170-1

US-08-991-170-1

US-08-991-170-51

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US-08-991-170-51

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APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAM-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08315468 Patent No. 5554534
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CLASSIFICATION: 424
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COUNTRY:
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US-08-315-468-3
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Sequence 3, A
Sequence 29, A
Sequence 1, A
Sequence 1, A
Sequence 1, A
Sequence 1, A
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Sequence 2,
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Biocceleration Ltd.
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(cgn2 6/ptodata/1/ina/1_COMB.seq:*

(cgn2 6/ptodata/1/ina/5_COMB.seq:*

(cgn2 6/ptodata/1/ina/6A_COMB.seq:*

(cgn2 6/ptodata/1/ina/6B_COMB.seq:*

(cgn2 6/ptodata/1/ina/H_COMB.seq:*

(cgn2 6/ptodata/1/ina/H_COMB.seq:*

(cgn2 6/ptodata/1/ina/PP_COMB.seq:*

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                                                                                        nucleic search, using frame plus p2n model
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US-10-089-678-2
US-10-089-678-3
US-09-661-322A-37
US-07-876-280-29
US-07-812-180A-1
US-08-315-468-1
US-07-941-650A-1
US-08-448-170-7
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Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0,
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Database:

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11 2 5 4 5 6 7 8 6

Result No.

Mon Jan

GAGTCATATAGCCATAGATTAGGTCATATTACATTTATT-----TACTCCAGT 1485 1486 TCAACTAGCACGTATGTACCTGTATTTTTTTGGACACACATCGGAGTGCAGATCTAACAAAT 1545 1048 ACAGITITATACAAAAAAGGTAGCTTCACTTCTGATCGTTATAGAGATATTGGGCTGGT 1107 1108 CATCAAATAAGCTATAAGCATATCGCTACGAGTÁGTACCTTTÁCÁCAGATGTATGGAACC 1167 AATCAAAATTTACAAAGTACTAGCAATİTİTGATİTİACGAÁTTACGATATTTACAAGACT 1227 1378 GATCGGACAAGAGATTCGGAATTAGAATTGCCTCCAGAAACTTCAGGTCAACAAATTAC 1437 451 ABNValProGlySerLeuArgTyrGluValProAlaABnLeuProSerGlnThrIleLeu 470 642 238 702 LeuGlnGlyLeulleArgGluTyrLysAspHisCyslleThrPheTyrAsnGlnGlyLeu 258 762 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278 822 882 ProLeuAlaValLygThrGluLeuThrArgGluValTyrThrAgpProValGlyPheThr 318 883 ccacrescaacaacagercagerracaagaaagrararacagareeaerrageegegra 942 338 ThralametGluasnasnalaargargargproSerTyrThrThrTrpLeuasnargIle 358 HisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyLys 396 ThraspSerlleThrProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerlle 416 Ser--------GluLeuProGlyLysAspLysProArgProAsnAla 483 524 ArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsnIle 543 GlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsnAsn IlevalaspasnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle CATTCCTTACAGTATATACAATGGCAGCAACCTACATTTACTTTATTAAGGGACGCA CAAATGAAACTTACTGCAGAATATTCTGACCACTGTGTAAAGTGGTATGAAACTGGTTTA MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr TyrileThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIleAsn LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrPhe PheValTyrThrArgThrLeuGlyAsnMetSerAsp---ValArgAsnIleTrpGlyGly TTATCAAATGGTGCAGTACTCCTTGATATAGTTTACCCTGGT------

US-10-782-096-2 (1-682) x US-10-089-678-2 (1-3504)	Qy 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArglleAsnSerAsnMet 22	OY 23 SerAbnCysTyrProLeualaLysAspProGlnMetThrMetArgAsnThr 42	OY 43 ABITYILYBGluTrpLeuAbimetCyBABpSerAbiThrGliPheileGlyAbpile 61	Qy 62 SerThrTyrSerSerProGlualaAlaLeuSerValArgAspAlaValLeuThrGlylle 81	Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeualaSerGlnSerPheGly 101	Qy 102 IleIleSerArgLeuIleGly1leLeuTrpalaGlyProAspProPheGluala 119	Qy 120 LeuwetValLeuValGluGluLeuIleLysEysSerIleAspGlnArgValArgGluAsn 139 :::	Gy 140 AlabeuargGluLeuGluGlyLeuGlnGlyIleMetargLeuTyrGlnThrargLeuGln 159	Qy 160 AlaTrpLeuValAenLy8AenAepAenArgArgAlaLeuValThrGlnTyrAla 178	Gy 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198	Oy 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218	Oy 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238	Gy 239 LeuGlnGlyLeuIleArgGluTyrLy8A8pHisCysIleThrPheTyrAsnGlnGlyLeu 258	Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278 1::::::::::::::::::::::::::::::::::::	Qy 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298 Db 820 ATGACATTACTGGTATTAGTAGCGTTATTTCCAAACTATGACACGTACGT	Cy 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318	319 GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnAsnThrThe	
Db 1546 ACAGTTAAAAGTGGCGAAATCACCCCAAATACCAGGGGCAAGTCTAGCACCATA 1599	Oy 544 GlyPheValileProGlyProThrGlyGsnLeuValLy8Val 558	Qy 559 SeraspSerTrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyr 576	Qy 577 ArgileArgLeuArgTyrAlaCysLeuValThrHisGlyAspAlailePheValGluHis 596	Qy 597 SerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611	Qy 612	Qy 628 AspValProGlyllePheThrProSerIleAsnProLeulleArgTyrArgThrGlnSer 647 :: :: ::	Oy 648 PheGlyThrHisAla	Qy 662 ABnThrPheProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeu 679 :::	Qy 680 Phelleasn 682 Db 2032 TTTACGAAT 2040	RESULT 2 US-10-089-678-2 ; Sequence 2, Application US/10089678				; NUMBER OF SEQ ID NOS: 3 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 2 ; LENGTH: 3504	TYPE: DNA ORGANISM: Bacillu FEATURE: NAME/KEY: exon	; IOCATION: (1)(3501) ; OTHER INFORMATION: US-10-089-678-2	5.76e-90 Length: 940.50 Matches:	Best Local Similarity: 36:1% Mismatches: 288 Query Match: 36:1% Indens: 56 DB: 3 Gaps: 23

TCAGAAGTCGAAAGCGCTGTAATTCGTTCACCACCTATTTGATATACTCAGTGAAATA 1056

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GENERAL INCORNATION:
APPLICANT: ASANO, Shinichiro
APPLICANT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
TITLE OF INVENTION: NOTION ORGANISM-CONTROLLING AGENT AND METHOD
FILE REFERENCE: 068021
CURRENT APPLICATION NUMBER: US/10/089,678
CURRENT PILLING DATE: 2002-04-03
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-08-03
RIOR APPLICATION NUMBER: PCT/JP01/06660
PRIOR PILLING DATE: 2000-08-03
RIOR PRIOR PILLING DATE: 2000-08-03
RECO TO NOS: 3
SEQ ID NOS: 3
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56
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Matches:
Conservative:
Mismatches:
Indels:
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                      Sequence 3, Application US/10089678
Patent No. 6962977
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GENERAL INFORMATION:
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APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupar, Mark J.
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APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Land Methods of Use
FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
CURRENT PILING DATE: 2000-09-13
SUPPHARE: Patentin version 3.0
SEQ ID NOS: 63
SOFTWARE: Patentin version 3.0
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|AGTGCA-----AATGAGTCTTTGACATCTCAATCATTTAGATTTTGCAGAATTTCCT 1815
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                                                                                                                                                   GTTAGATTTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGT 1308
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                          ProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIleGluSerLeuAlaArg 421
                                                                                                                                                                         460 ValProAlaAsnLeuProSerGlnThrIleLeu-----SerGluLeuProGlyLys 476
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|CTGTAAGA---TTATCATTCTTCTCGAGACGTATATTGGACTGAATCATATGCAGGA
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                                                                          422 IleTyrLeuGlyGlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSerArg
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APPLICANT: Payne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates
TITLE OF INVENTION: Controlling Acarides
NUMBER OF SEQUENCES: 30
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Patent No. 5262158
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                                                                                                                -----GTCCAAACGGGTATTAACATGGTAGA 195
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                                       99
                                                                                       ProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIleAsnSerValGlyThr 86
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                                       TrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSerThrTyrSerSer
                                                              -----retttgtgtatageegagegaataatatcaatecaettgttagegeatcaaea
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 ACACAAATGGATCTATCACCAGATGCTCGTATTGAGGAT-
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                      LeuMetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
                                                                                                                                                                                                  460 GATTGGCTGGAAAATCGCAATGATGCAAGAACTAGAAGTGTTGTTTCTAATCAATTTATA 519
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                                                        340 ATTATGGAACGAGGAAGAACTCGTTGATCAAAAATAGAAAATATGTAAAAGATAAG 399
                                                                                               140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
                                                                                                                                   400 GCTCTTGCTGAATTAAAAGGGCTAGGAAATGCTTTGGATGTATATCAGCAGTCACTTGAA 459
                                                                                                                                                                            160 AlarrpieuValAsniysAsnAspAspAsnArgArgAlaLeuValThr---GlnTyrAla 178
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249
113
267
105
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                                                                                                                                                                COMPUTER: IBM-PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,280
FILING DATE: 19920430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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IMMEDIATE SOURCE:
CLONE: E. COLI NM522 (PMYC2320) NRRL B-18769
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                : David R. Saliwanchık
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                 FILING DATE: 19920430
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: Saliwanchi, 1794
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 104
TELEFAN: 904-375-8100
TELEFAX: 904-375-8100
TELEFAX: 904-375-8100
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TELEFAX: 904-375-8100
TELEFAX: 904-375-8100
TELEFAX: 904-375-8100
TENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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STRAIN: kumamotoensis
                                  STREET: 2421 N.W. 418t Str
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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901.50
49.3%
33.9%
25.1%
CORRESPONDENCE ADDRESS: ADDRESSE: David R.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
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Pred. No.:
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Best Local Similarity:
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APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: A No. 3366892el Coleopteran-Active Bacillus
TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding
TITLE OF INVENTION: Coleopteran-Active Toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1582 CAAATTCCAGCGGTAAAGGGAGACATGTTATATCTAGGGGGTTCC-----GTAGTA 1632
                                                                                                                                                                                                                                                                                                                                          .633 CAGGGTCCTGGATTTACAGGAGGAGATATATATAAAAAGAACCAATCCTAGCATATTAGGG 1692
                                                                                                                                                                                                                                                                                                                                                                                                        1693 ACCTTTGCGGTTACAGTAAATGGGTCGTTATCACAA---AGATATCGTGTAAGAATTCGC 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1750 TATGCCTCTACAACA-----GATTTTGAATTTACTCTATACCTTGGCGACACATA 1800
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                                                                              1462 CATATTACCTCCCATTCTTTCTCTAAAATGGGAGTGCATACTATGGGAGTTTCCCTGTA 1521
                            1345 TTATATTCAAAAACACATACAGCTCTCCAAGGGTGTACACAGGTTTATGAATCAAGTGAT 1404
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                                                                                                                                                                                                                                                          GinileAspAlaValLysGly------TrpGlyGlyAsnIleGlyPheValIle 547
                                                                                                                                                                                                                                                                                                                         548 ProGlyPro-----ThrGlyGlyAsnLeuValLysValSerAsp------Fer 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                    582 TyralaCysLeuValThrHisGlyAspAlaIlePheValGluHisSerGlySerSerHis 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 IleValSerPhePheAspCysSerAsnSerSerGlyArgProSerAsnThrLeuLeuGlu 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----IleAspLysPheGluPheIleProLeuAsn---ThrPhe---ProAsnGlnSer 668
---3er 471
                                                                                                                          TyrileSerAsnPheAspAlaArgArgSerSerSerGlyGlyIleValSerLeuLeuThr 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622 SerAspPheArgTyrIleAspValProGlyIlePheThrProSerIleAsnProLeuIle
                                                                                                                                                                                                                                                                                                                                                                                      562 TrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArg
                                                            GluLeuProGlyLysAspLysProArgProAsnAlaGlyAspPheSerHisArgLeuSer
                                                                                                                                                                                          PheGlyTrpAlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspLysIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                642 ArgTyrArgThrGln-----SerPheGlyThrHisAla-----
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STREET: 2421 N.W. 41st Street, Ste A-1
CITY: Gainesville
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Patent No. 5366892
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Roman Sal:
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STATE: FL
COUNTRY:
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102 IlelleSerArgLeulleGlyIleLeuTrpAlaGlyPro-----AspProPheGluAla 119
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61 TCCAGTGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAGATGCGTTACAAATATG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 GGCATTGTTGGTCGAATACTAGGAGCTTTAGGGGTTCCATTTGCTAGTCAGATAGCTAGT 279
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249
1113
267
105
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,180A
FILING DATE: 19920102
CLASSIFICATION: 435
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Mismatches:
Indels:
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LIBRARY: FONCERRADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-782-096-2 (1-682) x US-07-812-180A-1 (1-3471)
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Matches:
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ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, Roman
TELECOMUNICATION INFORMATION:
TELEPHONE: 904-372-5800
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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|2004 TCATTIGCACTIGAGGATAGGGATATITTTGAAATTAATTCAACTGIGGGAAACTAGCT 1263
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                                                                                                                                                                                                                                                                                                                              669
520 GCTTTAGATCTTTAACTTTGTTAGTTCCATCTTTTGCAGTATCCGGACAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATAAATTGAAAGGTACCACTTCTAAAAGTTGGCTGAATTATCATCAGTTCGGTAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                               239 LeuGlnGlyLeulleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                       259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThe
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                                                                                              IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle
                                                                                                                                                                                       LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla
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640 TCTATTTTGGAGAGAGTGGGGATTTACACCAGGTGAAATTTCTAGATTTTATAATCGT
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|174 AATTACGGTCGAATCACTTCA-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 TTCTATAGTTTCATTGTTGGTCAATTATGGCCGTCAAAGAGCGTAGATATATGGGGAGAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:::
61 TCCAGTGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAGATGCGTTACAAAATATG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 GGCATTGTTGGTCGAATACTAGGAGCTTTAGGGGTTCCATTTGCTAGTCAGATAGCTAGT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuMetValLeuValGluGluLeuIleLysLysSerileAspGlnArgValArgGluAsn 139
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249
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Mismatches:
Indels:
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ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kunamocioensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF LUIS
LIBRARY: FONCERRADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-782-096-2 (1-682) x US-08-315-468-1 (1-3471)
              PRIOR APPLICATION DATA:

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APPLICATION NUMBER:

NAME:

REGISTRATION NUMBER:

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REBERNORE, DO4-372-5800

TELEPAN:

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  APPLICATION NUMBER:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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220 GGCATTGTTGGTCGAATACTAGGAGCTTTAGGGGTTCCATTTGCTAGTCAGATAGCTAGT 279
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340 ATTATGGAACGAGGAAGAACTCGTTGATCAAAAAATAGAAAAATATGTAAAAGATAAG 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 SerThrTyrSerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 AsnTyrLysGluTrpLeuAsnMetCys---AspSerAsnThrGlnPhelleGlyAspIle 61
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Matches:
Conservative:
Mismatches:
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IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC1638), NRRL B-18751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-782-096-2 (1-682) x US-07-941-650A-1 (1-3471)
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PRICING DATE: 21-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,112
FILING DATE: 16-7AN-1991.
NAME: SAliwanchik, David R.
REGISTRATION NUMBER: 31,794
TELECOMMUNICATION INFORMATION:
TELEFAN: 904-375-8100
TELEFAN: 904-375-8100
TELEFAN: 904-375-8100
TELEFAN: 914-372-5800
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTER:STICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Bacillus thuringiensis STRAIN: kumamotoensis
                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
ANTI-SFNEC
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901.50
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Best Local Similarity:
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         532 GinileAspAlaValLysGly------TrpGlyGlyAsnIleGlyPheValile 547
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                                                             PheGlyTrpAlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspLysIleThr
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APPLICANT: Uyeda, Kendrick A.
APPLICANT: Uyeda, Kendrick A.
APPLICANT: Bradfisch, Gregory A.
TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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CLASSIFICATION: 435
PRIOR APPLICATION DATE: 435
APPLICATION NUMBER: US 07/758,020
FILING DATE: 12-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/658,935
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STATE: FI
COUNTRY:
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                                                                                            913 TTTGCAAGTACGAATTGGTTTAATAATAATGCACCATCGTTTTCTGCCATAGAGGCTGCC
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                   TrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArgLeuGlnGlyLeuIleArg
                                                                           GluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeuAsnGlnPheAsnArgSer
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| ATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGTTTTTATAGTTTTTCTT
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Matches:
Conservative:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFTCATION: 424
ATTORNEY/AGENT INCREMATION:
NAME: Saliwanchik David R.
REGISTRATION NUMBER: 31,794
TELECOMMUNICATION INFORMATION:
TELEFRNCE/DOCKET NUMBER: M/S 102D.C1
TELEFRNICATION INFORMATION:
TELEFRNICATION NUMBER: M/S 102D.C1
TELEFRNICATION NUMBER: M/S 102D.C1
TELEFRNICATION NUMBER: M/S 102D.C1
TELEFRNICATION NUMBER: M/S 102D.C1
TELEFRNICATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTER STICS:
LENGTH: 3684 base 'paire
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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Mismatches:
Indels:
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Matches:
REFERENCE/DOCKET NUMBER: M/S 102DCD1
               TELECOMMUNICATION INFORMATION
TELEPHONE: (352) 375-8100
TELEPAX: (352) 372-8100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3664 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Cummings, David A.
APPLICANT: Cummings, David A.
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Stelman, Steve
ITILE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
ITILE OF INVENTION: Encoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
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1807 TTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATAAGTAATAAT 1866
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   572 ArgGlnThrSer-----TyrArgIleArgLeuArgTyrAlaCysLeuValThrHis 588
                                                                          GlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPheAspCys
                                                                                                                                                 SerAsnSerSerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAsp
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: POPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/961,803
FILING DATE: 31-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 31-OCT-1997
CLASSIFICATION NOTES.

PRIOR APPLICATION BOTH:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-UUNE-1993
CLASSIFICATION: 800
PRIOR APPLICATION BATE:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/448,170
FILING DATE: 23-MAY-1995
CLASSIFICATION: 800
ATTONEY/AGENT INFORMATION:
NAME: SANGE'S, Jay M.
REGISTRATION NUMBER: 39,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08961803
Patent No. 6150589
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Best Local Similarity:
Query Match:
DB:
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                                                                                                  313 TITGCAAGTACGAATIGGTTTAATAATAATGCACCATCGTTTTCTGCCATAGAGGCTGCC 972
                                                                                                                                                                                                                              LeuGlyAsnMetSerAspValArg-----AsnIleTrpGlyGlyHisThrLeuValGlu 382
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GAATATTCTGATTATTGCGCAAGATGGTATAATACGGGTTTAAATAATTTGAGAGGGACA 735
                                AspleuAlaIleleuPheProAsnTyrAspProArgArgTyrProLeuAlaValLysThr 304
                                                                                                                                             325 GlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPheThrAlaMetGluAsnAsn 344
                                                                                                                                                                                    345 AlaArgArgArgProSerTyrThrThrTrpLeuAsnArgIlePheValTyrThrArgThr 364
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                                                                         GlyAspAlallePheValGluHisSerGlySerSerHisIleValSerPhePheAspCys
                    AsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAspMetThrLeuThrValLeu
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APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
                   112 AGCTTGTGTATAGCCGAGGGAAC-------------AATATCGATCCATTGTTAGC 156
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                                                                               629 ValPro------GlyllePheThrProSerileAsnProLeuIleArg
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SerAsnSerSerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAsp
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Patent No. 6593293
GENERAL INFORMATION:
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APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William
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--LeuProSerGlnThrIleLeuSerGluLeuPro
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STATE: NC
COUNTRY: USA
ZIP: 27709
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                                                 GluLeuileLysLysSerIleAspGlnArgValArgGluAsnAlaLeuArgGluLeuGlu 145
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           IleGlyIleLeuTrp---AlaGlyProAspProPheGluAlaLeuMetValLeuValGlu 125
                                                                 GlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGlnAlaTrpLeuValAsnLys 165
                                                                                                                                      AsnAspAspAsnArgArgAla---LeuValThrGlnTyrAlaIleValAspAsnPhePhe 184
                                                                                                                                                                                          CITAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCATTATTAATGGTATAT 555
                                                                                                                                                                                                                        AlaGinAlaAlaAsnLeuHisLeuIeuLeuLeuArgAspAlaAspTyrPheGlyAlaGln 224
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616 TITGGGCTTACATCCCAAGAAATTCAACGTTATTATGAGGGCCAAGTGGAAAAAACGAGA 675
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                                                                                                                                                                                                                                                                                                                              GAATATICIGATIATIGCGCAAGAIGGIATAATACGGGITTIAAATAATTIGAGAGGGACA 735
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                      GATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGGCTTAGAACTTGATTTT
                                                                                                                                                                               GluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeuProValTyr
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                                                                                                                 GĠŦŤŦÄGGAAATTCCTŦŦÄĠĠCCTÄŤĊÄÄCAGTCAĊŦŦĠAAGAŦŦĠĠĊŦÄGAAÄÄĊĊĠŦ
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|-----GTCCTGAGGGTAACTGTCGGAGGAGTACTTTTGATCAAGGATTCCCTAGT 1755
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                                                                                                                                                                                                                                                                                                                                                                                      ACGCACCGTAGTGCAGATCGTACCATTAGTTCAGATAGCATAACAAAATACCA 1521
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                                                                GlyLysAspLysProArgProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSer 494
                                                                                                                                                                                                                                                                                                                            AlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspLysIleThrGlnIleAsp 534
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                                                                                                      -----GAATTACCA
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Patent No. 6121521
GENERAL INFORMATION:
APPLICANT: Desai, Nalini
TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121521artis Corporation
STREET: 3054 Cornwallis Rd.
   GGGTATACTGGAGTGGGGACACAACTATTTGATTCAGAAACT
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ZIF: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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1067 ACCATCCAGTCTAGACCCATCGGCGGCGGCCTGAACACCAGCACCCACGGCGCCACCAAC 1126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 GlyvalSerArgvalIlePheAsnThrSerAsnIleAsnAsnValPro-----GlySer 455
                                              LeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAlaAspTyr 220
                                                                                                                                                                                                                                                                                               LeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyrProLeu 300
                                                                                                                                                                                                                                                  TAAGGGGCACCAACCGCCAGCTGGGTGCGCTACAACCAGTTCCGCCGCGACCTGACCACTGACC
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                                                                ThrLeuValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyLySThrAsp
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                                                                                                           PheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArgLeuGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 GCCGAGGGCAACAACATCGACCCCTTCGTGAGCGCCAGCACCGTGCAGACCGGCATCAAC 178
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                                                                                                                                                                                                                                                                                                                                                                                                                          containing coding sequence for hyFLIB protein'
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 8854
OTHER INFORMATION: /note= "Sequence of pCIB5520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                               LOCATION: 11..3694
OTHER INFORMATION: /product= "hyfLIB protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-782-096-2 (1-682) x US-09-053-549-1 (1-8854)
APPLICATION NUMBER: US/09/053,549
FILING DATE: 01-APR-1998
CLASSIPTCATION: 800
ATTOCNEY AGENT INFORMATION:
NAME: Pace, Gary M:
REGISTRATION NUMBER: 40,403
REGISTRATION NUMBER: GGC 1995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 1919-541,4959
TELEFAX: 919-541-8689
                                                                                                                                INFORMATION FOR SEQ 11 + 9582

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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892.00
50.2%
36.5%
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OTHER INFORMATION:
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
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Pred. No.:
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US-09-053-549-1
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                                IleGlyIleLeuTrp---AlaGlyProAspProPheGluAlaLeuMetValLeuValGlu 125
                                                                                                                                                                                                                                                                                                                                                                                      GGACTTGGAAACTCTTTCAGAGCTTACCAACAATCTCTTGAGGATTGGCTTGAGAACAGA 435
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                                                                                                                              67 ProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIleAsnSerValGlyThr
                                                                                                                                                         IleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGlyIleIleSerArgLeu
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                ProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThrAsnTyrLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeuLeuProValTyr
                                                                        47 TrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSerThrTyrSerSer
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                                                                                 566 LysValGlnAlaProGlnArgGlnThrSerTyrArglleArgLeuArgTyrAlaCysLeu 585
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US-09-178-25-22
| Sequence 22, Application US/09178252
| Patent No. 6218188
| Fatent No. 6218188
| GENERAL INFORMATION:
| APPLICANT: Cardineau, Guy A. APPLICANT: Cardineau, Steven J. APPLICANT: Narva, Kenneth E. TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins | FILE REFERENCE: MA-714XCZ | CURRENT APPLICATION NUMBER: US/09/178,252 | CURRENT FILING DATE: 1998-10-23 | EARLIER APPLICATION NUMBER: 60/065,215 | EARLIER PILING DATE: 1997-11-12 | EARLIER PILING DATE: 1998-03-02 | NUMBER OF SEQ ID NOS: 27 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NO 22 | LENGTH: 3558 | LENGTH: 3558
                                             ||||
|TICAACTICGAC-----TTCTTCGTGAGCCGCGGCGGCACCACCTCGTGAACTICCGC
                           550 ProThrGlyGlyAsnLeuValLysValSerAspSerTrpHis------SerLeu
                                                                                                                                           ValThrHisGlyAspAlallePheValGluHisSerGlySerSer---HisIleValSer
                                                                                                                                                                                                                                                        -----ArgTyrIleAspValProGlyIlePheThrProSerIleAsnProLeuIleArg
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Conservative:
Mismatches:
Indels:
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107 IleGlyIleLeuTrp---AlaGlyProAspProPheGluAlaLeuMetValLeuValGlu 125
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FILE REPERENCE: MA-714XC2D1
CURRENT APPLICATION NUMBER: US/09/826,666
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/178,252
PRIOR PILING DATE: 1998-10-23
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 22
LENGTH: 3558
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    AsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyLysThrAsp---SerIleThr 401
                                                              ProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIleGluSerLeuAlaArg
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US-09-826-660-22
Sequence 22, Application US/09826660
Sequence 22, Application US/09826660
GENERAL INFORMATION:
APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
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                                                                GlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.0.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PEFEROEN, Marnix
APPLICANT: JANSENS, Stefan
APPLICANT: DENOLE, Peter
TITLE OF INVENTION: CONTROL OF OSTRINIA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: US 07/938,362
FILING DATE: 31-AUG-1992
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/164,781
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STRAIN: entomocidus HD 110
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08377690 Patent No. 5628995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4074 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113
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3: DNA (genomic)
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MEDIUM TYPE: Floppy disk
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STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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STRANDEDNESS: double
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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MOLECULE TYPE: DN
ORIGINAL SOURCE:
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TTCGGACTTACTTCTCAAGAGATTCAAAGATACTACGAGAGACAAGTTGAGAAGACTAGA
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NAME/KEY: CDS
LOCATION: 186..3872
COTHER INFORMATION: /note= "PROPERTIES: CrylB is toxic OTHER INFORMATION: Ostrinea nubilalis (among others)"
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Matches:
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DB:
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APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Xiang Feng
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
ITILE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
ITILE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
NUMBER OF FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 77,
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Publication No. US20020151709A1
GENERAL INFORMATION:
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| NAME/KEY: misc_feature
| LOCATION: (0)...(0)
| COTHER INFORMATION: CFy1218-1
| US-10-032-717-1
LENGTH: 3621
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Command line parameters:

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-DB=Published Applications|NA Main -QFMT=fastap -SUFFIX=p2n.rnpbm
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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE-pct
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-HRAPSIZE=500 -MINLEN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pto -NORM=ext
-HSRENSIO782056 @CGN 1 1 1026 @runat 20012066 095216 24424 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -MAIT -DSPBLOCK=100 -DEV_TIMEOUT=120 -WARN TIMEOUT=30
-THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
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              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                 OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-032-717-1
US-10-44-637-1
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Maximum Match 100%
Listing first 45 summaries
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Result

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|GTATACACAATCAAGAAGCATTTCTTCCGCTCGCTATATAAGACAT---TGGGCT 1104
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GGAAACGAAAGCACAACTAACAAGGGAAGTATATACAGATCCACTGGGCGCGCGTA 942
                                             lleuGluSerglyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338
                                                                                          Grcrrcaarregircc-----regraficac---aaagcaccrrcrrrc 987
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GGAGTGATAGAATCATCGTTATTCGACCACCCCATGTATTTGATTATATAACGGGACTC 1047
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|GTCATCAAATAAGCTACCATCGTGTCAGTAGGGGTAGTAATCTTCAACAAATGTATGGA 1164
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                                                                                                                                                    140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
                                                                                                                                                                                                                                                                  160 AlaTrpLeuValAsnLysAsnAspAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 PhevalTyrThr----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
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                                                                                                                                120 LeumetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 703 CAAATGAAACTTACTGCAGAATATTCTGATCACTGTGTAAAGTGGTATGAAACTGGTTTA 762
 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla
                                                                102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla
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| ATCCTGGATAGTTTATTTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTA
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                  681
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Sequence 1, Application US/20414637
Publication No. US2003017752841
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Alang Feng
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Simg
TITLE OF INVENTION: Genee Encoding No. US20030177528A1e1 Proteins With
TITLE OF INVENTION: Peeticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
PRIOR PAPLICATION NUMBER: US/10/032,717
PRIOR PAPLICATION NUMBER: 60/242,838
PRIOR PAPLICATION NUMBER: 60/242,838
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 AGTCCAAATAATCAAAATGAAATATGAAATTATAGATGCGACACCT---TCTACTTCTGTA 60
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                                                               ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPhelle
---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn---
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
OKGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
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Best Local Similarity:
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TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal TITLE OF INVENTION: Activity FILE DE INVENTION: Activity FILE REFERENCE: 357108/263940 CURRENT APPLICATION NUMBER: US/10/606,320 CURRENT FILING DATE: 2003-06-25 PRIOR APPLICATION NUMBER: 60/391,786 PRIOR PILING DATE: 2002-06-26 PRIOR PILING DATE: 2002-06-26 PRIOR FILING DATE: 2003-04-04 NUMBER OF SEQ ID NOS: 134 SUPERIOR FILING DATE: 2003-04-04 SUPERIOR FILING DATE: RESEQ for Windows Version 4.0
                                                                                                                                                                                                       TYPE: DNA ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                            ; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry1218-1
US-10-606-320-1
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LOCATION: (1)...(3621)
FEATURE:
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Best Local Similarity:
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                  1276 ---TATATATTT----TTTGGAATGCCAGAAGTTGGTTTTTTCATGGTAAACCAATTG 1326
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603 TTACCGTTTGTTCCAGTGGTAAAAGGACCAGGACATACAGGAGGGGATTTATTACAGTAT 1662
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| AATAATACCAGAAAGACGTTAAAGTAT------AATCCAGTTTCCAAAGATATT 1374
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1375 ATAGCGAGTACAAGATTCGGAATTAGAATTACCTCCCAGAAACTTCAGATCAACCAAAT 1434
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AsnryrileThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnfle 449
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                                                          AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle
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Length:
Matches:
Conservative:
Mismatches:
Indels:

3.04e-96 948.00 50.9% 34.4%

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GCGCTTTCGGAATTAGAAGGATTAGGTAATAATTACCAATTATATCTAACTGCGCTTGAA 462
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|163 GAATACCCTGGTTCACCTGAAGTACTTGTTAGCGGACAAGATGCAGCTAAGGCCGCAATT 222
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                                                                                                          SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
                                                                                                                                                                                                                                                        63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
                                                       43 AsnīyriysGluTrpieuAsnMetCysAspSerAsnThrGlnPhelleGlyAspIleSer
                                    SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArglleAsnSerAsnMet
US-10-782-096-2 (1-682) x US-10-606-320-1 (1-3621)
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Sequence 1, Application US/10606320
Publication No. US20040091505A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn

Rafael Herrmann Theodore W. Kahn Albert L. Lu Billy Fred McCutchen James K. Preenail James F.H. Wong

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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1603 TTACCGTTTGTTCCAGTGGTAAAAGGACCAGGACATACAGGAGGGATTTATTACAGTAT 1662
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                                                                                                                                                                                                                                                                                                            592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
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                                                                                                                       ------GlnAlaProGln
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Publication No. US20040210963A1

GENERAL INFORMATION:

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Activity

FILE REFERENCE: 35718/368350

CURRENT FILING DATE: 2003-06-26

PRIOR PELICATION NUMBER: 60/491,786

PRIOR PELICATION NUMBER: 60/460,787

PRIOR PELICATION NUMBER: 60/460,787

PRIOR PELICATION NUMBER: 10/606,320

PRIOR PELICATION NUMBER: 10/606,320
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Matches:
Conservative:
                                                                                                                     559 SerAspSerTrpHisSerLeuLysVal------
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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FEATURE:
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| BATAATACCAGAAAGACGTTAAAGTAT------AATCCAGTTTCCAAAGATATT 1374
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Oy 339 ThralaMetGluAsnAsnAlaArgArgArgPrOSerTyrThrTrpLeuAsnAsnIle 358 11		0y 416 IleGluSer	Db 1276TAINATTTTITICHATCCCAGAAGICGAGTTTTTCATGGTAAACCAATTG 1326 Qy 450 ASHASIVAIPTGIYSELEUAGTYTGIUVAIPTOALAASILEUPTOSETGITHTILE 469 Db 1327 AATAATACCAGAAAGACGTTAAAGTATAATCCAGTTTCCAAAGATATT 1374	470 LeuSerGluLeuProGlyLysAspLysProArgProAser ::::::::::::::::::::::::::::::::::::	Oy 483 AlaGlyAspheSerHisArgleuSerTyrIleSerAsnPheAspAlaArgArgSerSer 502 :::		Oy 543 IleGlyPheValIleProGlyProThrGlyGlyAsnLeuValLysVal 558		1723		Db 1813 ACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCAGATGCTATCACA 1872 Qy 632 IlePheThrProSerIleAsnProLeulleArgTyrArg	Oy 645ThrGlnSerPheGlyThrHisAlalleAspLysPheGluPheIleProLeuAsn 662
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Best Local Similarity: 34.4\$ Mismatches: 276		163	GATATAGTAGGTAAATTACTATCAGGTTTAGGGGTCCCATTTGTTGGGCCCATAGTAGGTTAGGGGTTTAGGGGTCCCATTTGTTGGGCCCATAGTGGGTTTAGGGTTTAGGGGTCCCATTTGTTGGGCCCATAGTGAGTTTAGTTGGGCCCATAGTGAGTTTAGTTGGGCCCATAGTGAGTTTAGTTGGGCCCATAGTGAGTTTGTTGGGCCCATAGTGAGTTAGTT	283 120 343	140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln	Cy AlalraceuvalAssunysAsanaspasDasDasDasDasDasDasDasDasDasDasDasDasDa	199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla	219 AspTyrPheGlyalaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg	239 LeuGlnGlyLeulleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu	<pre>Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278 ::: ::: </pre>		31 9 94 3

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ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPhsIle
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                                                                                                                                                                                                                           of Insect
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Matches:
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                                                                                                 Sequence 5, Application US/11021115
Publication No. US20050166284A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-11-021-115-5
                                                                                                                                 APPLICANT: Abad, Andre
APPLICANT: Flannagan, Ronald
APPLICANT: Herrmann, Rafael
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ATAGCGAGTACAAGAGTTCGGAATTAGAATTACCTCCCAGAAACTTCAGATCAACCAAAT 1434
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160 AlaTrpLeuValAsnLysAsnAspAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
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|------aataataccagaaagacgttaaagtat------aatccagtttccaaagatatt
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1993 ACATATGAAGCGGAACAAGATTTAGAAGCAGCGGAAGAAAGCAGTGAATGCCTTGTTTACG 2052
               1813 ACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCAGATGCTATCACA 1872
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                                                                                                                                                   IleGlyPheValIle------ProGlyProThrGlyGlyAsnLeuValLysVal 558
                                                                                                                                                                                                    -----GlnAlaProGln 571
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US-10-032-717-27
Sequence 27, Application US/10032717
Fublication No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Andre R. Abad
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Preadore W. Kahn
APPLICANT: Preadore W. Kahn
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APPLICANT: Preadore W. Kahn
APPLICANT: Preadore W. Kahn
APPLICANT: Uynn E. Sime
TITLE OF INVENTION: Peericidal Activity Against Coleopterans
TITLE OF INVENTION: Peericidal Activity Against Coleopterans
TITLE OF INVENTION NUMBER: 05/10/032,717
CURRENT FILING DATE: 2000-10-24
FRIOR PALLICATION NUMBER: 60/242,838
PRIOR PLING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
LENTH: 4874
 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer 502
                                                                                                                                                                                                                                                                                                   592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
                                                                                                                                                                                                                                                                                                                                                    SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
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                                                 SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn
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ORGANISM: Bacillus thuringiensis
FEATURE:
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953 GATATAGTAGGTAAATTACTATCAGGTTTAGGGCTCCCATTGTTGGGCCGATAGTGAGT 1012
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TCCAATGATTCTAACAGATACCCTTTTTGCGAATGAGCCAACAAATGCGCTACAAAATATG 850
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| 1373 TCAATTTTTGGAGAAGAAGAAGGTGAAGGTCAACTACTATTAATAACTATTATGATCGT
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Matches:
Conservative:
Mismatches:
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Gaps:
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-10-032-717-27
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Pred. No.:
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2663 AATTCAACATTATCTGGTATAGTTTACGTTGACGAATCGAATTCATCCCAGTAGATGAG
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2603 ACATTAAATTTAGCAACAGATAGTTCGCTAGCATTGAAACATAATTTAGGTGAAGACCCT 2662
                                                                                                                                                                         663 ThrPhe---ProAsnGlnSerLeuGluLy8ArgGluGlnGluValAsnAspLeuPheIle 681
                                                                                                645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xiang Feng
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
TITLE OF INVENTION: Besticidal Activity Against Coleopterans
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/414, 637
CURRENT FILING DATE: 2001-0-24
PRIOR PAPLICATION NUMBER: 60/242,838
PRIOR PILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
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Mismatches:
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OTHER INFORMATION: Genomic DNA 1218-1
                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 27, Application US/10414637; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Wicholas B. Duck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bacillus thuringiensis
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Best Local Similarity:
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1673 AACGIGICTICAAITGGITCC------IGGIAIGAC---AAAGCACCTICTITC 1717
                                                                                                                                                                                                                     1718 GGAGTGATAGAATCATCCGTATTCGACCACCCCATGTATTGATTATAAAACGGGACTC 1777
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(895 ACTAATCAAAATCTACACACACTAGTACCTTTGATTTTACGAATTATGATATTTACAAG 1954
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2105 ATAGCGAGTACAAGATTCGGAATTAGAATTACTCCCAGAAACTTCAGATCAACCAAAT 2164
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2333 TIACCGITIGITÇCAGIGGIAAAAGGACCAGGACAIACAGGAGGGGAITIAITACAGATAI 2392
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                                                                                                              319 GlyvalLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338
                                                                                                                                                                                             339 ThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrTrpLeuAsnArglle 358
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                                      ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr
                                                            377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly
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431 AsnTyrileThrSerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnIle	Db 2057 AATAATACCAGAAAGACGTTAAAGTATAATCCAGTTTCCAAAGATATT 2104 Qy 470 LeuSerGluLeuProGlyLygABpLygProArgProAsn 482	483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer :::	Oy 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisTnrSerMetAspArgAsm 522 :::		Db 2333 TTACCGTTTGTTCCAGTGGTAAAGGACCAGGCATACAGGGGATTTATTACAGTAT 2392 Qy S59 SerAspSerTrpHisSerLeuLysValGlnAlaProGln 571 ::: ::: :::	Qy 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591 :::	592 IlePheValGluHisSerGlySerSerHisIleValSerPheAbpCysSerAsnSer	2543	83Z ILEPHEINIKPOSETILEANIKPOSETILEAKSIYANGS	645Intoinserpreditionaliteaspuysrecturiterierrobenser :::::	Db 2723 ACATATGAAGAGAACAAGATTTAGAAGAGAAGAAGAAGAAGAAGAAGAAGAAGAA	2783 AAT	RESULT 8 US-10-606-320-17 ; Sequence 17, Application US/10606320 ; Publication No. US20040091505A1 ; GENERAL INFORMATION:	; APPLICANT: Andre R. Abad ; APPLICANT: Ronald D. Flannagan ; APPLICANT: Rafael Herrmann ; APPLICANT: Theodore W. Kahn	; APPLICANT: Albert L. Lu ; APPLICANT: Billy Fred McCutchen ; APPLICANT: James K. Presnail
893 GAATACCCTGGTTCACCTGAAGTACTTGTTAGCGGACAAGATGCAGCTAAGGCCGCAÅTT 952 82 A8nSerValG1yThr1leLeuSerAsnLeuG1yValProLeuAlaSerG1nSerPheG1y 101 11:	1013 CTTTATACTCAACTTATTCTTTCTGTGGCCTTCAGGGGAAAAAGGGGAAATT 1072 120 LeumetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139 1073 TTTATGAACAAGAACTGATTATTATCAAAATAGGAAAATATGAAAAAAAA	AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln GGCTTTCGGAATTAGAAGGATTAGGTAATAATTACCAATTATATATA	160 AlarrpLeuValAbnLysAsnAspAspAsnArgArgAlaLeuValThrGlnTyrAla 178 	179 IleValAapAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198 ::: ::: ::: ::: ::: ::: ::: ::: :::		1373 TCAATTTTGGAGAATGGGGATGGTCAACAACTACTATTAATAACTATTATGATGT 1432 239 LeuGlnGlyLeulleArgGluTyrLysAspHisGysIleThrPheTyrAsnGlnGlyLeu 258 1433 CAAATGAAACTTACTGCAGAATATTCTGATCACTGTGAAGTGGTAAGGTATGAAACTGGTTAA 1492	ABIGInPheAsinArgSerAsinAlaGlnAspTrpValSerPheAsinArgPheArgThrAsp::::::::: ::: ::: 	279 MetThrLeuthrValLeuaspLeualaileLeupheProasnTyraspProargargTyr 298 	299 ProLeuAlaValLygThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318 ::: :::	319 GlyvalLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338 	339 ThralaMetGluAsnalaArgArgArgArgProSerTyrThrThrTrpLeuAsnargIle 358 	359 PhevaltyrThrArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376	377 GlyhisThrLeuValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395 ::: 1835 GGTCATCAATAAGCTACCATGGGGTAGGGGTAGTAATCTTCAACAAATGTATGGA 1894	396 LygThrAgpSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415 	416 IleGluSerLeuAlaArgIleTyrLeuGlyGlyThrGluAlaAen 430

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1835 GGTCATCAAATAAGCTACCATCGTGTGGTAGGTAGTAATCTTCAACAAATGTATGGA 1894
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      GCAAAATTAAAAGGCACGAGGGCTAAAACAATGGGTTGACTATAACCAATTCCGTAGAGAA
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|AATACAATATATTCAGATAAAATCACTCAAATTCCGGCCGTTAAATGTTGG---GATAAT
                                                                                                                                                                      1433 CAAATGAAACTTACTGCAGAATATTCTGATCACTGTGAAAAGTGGTATGAAACTGGTTTA
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                                                                     AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg
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TSS ATCCTGGATAGTTTTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTA 1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
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APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
                                                                                                                                                                                                                                                                                                                                                                                                     4874
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Matches:
Conservative:
Mismatches:
Indels:
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                                        FILE REFERENCE: 35718/363948

CURRENT APPLICATION: Activity
FILE REFERENCE: 35718/363948

CURRENT APPLICATION NUMBER: US/10/606,320

CURRENT PILIUG DATE: 2003-06-25

PRIOR PILIUG DATE: 2002/66-26

PRIOR PILIUG DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 134

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 4874
                                                                                                                                                                                                                                                                                                                  LOCATION: (0)...(0)
OTHER INFORMATION: Genomic DNA 1218-1
                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Bacillus thuringiensis
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948.00
50.98
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Best Local Similarity:
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                  SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet
                                                                             SerAsnCysTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr
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                                                                                                                                     AAAGCAGGGAAATATCGTGTAAGACTGAGATATGCTACT------GATGCA 2497
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                                                                                                                                                                                                                            SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrlleAspValProGly 631
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                                                                                                                                                                                                                                                                                                                                                                   ---GlnAlaProGln
                                                                          AATAGAAGTACTGGTTCTGGAACCTTATTTCTAGCTCGATATGGCCTAGCATTAGAA
                                                                                                                                                                                                                                                                                       IlePheThrProSerIleAsnProLeuIleArgTyrArg---------
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Publication No. US20040210963A1

GENERAL INFORMATION:

APPLICANT: Albert L. Lu

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Activity

FILE REFERENCE: 35718268350

CURRENT APPLICATION NUMBER: US/10/746,914

PRIOR PELING DATE: 2003-12-24

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2003-06-26

PRIOR FILING DATE: 2003-06-26

PRIOR FILING DATE: 2003-06-26

PRIOR PELING DATE: 2003-06-25

NUMBER OF SEQ ID NOS: 143

SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
                                                SerAspSerTrpHisSerLeuLysVal---
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LOCATION: (0)...(0)
OTHER INFORMATION: Genomic DNA 1218-1
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ORGANISM: Bacillus thuringiensis
FEATURE:
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Query Match:
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US-10-746-914-17
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Sequence 2, Application US/10089678
Sequence 2, Application US/10089678
Publication No. US2030017967A1
GENERAL INFORMATION:
APPLICATT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
TITLE OF ILLING DATE: 2002-05-05-05
CURRENT FILIANG DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 3
SOFTHARE: PATCHLIN VERSION 3.1
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US-10-089-678-2
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                                                                                                                                                                                        416 IleGluSer-------LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
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PheValTyrThr ----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
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                                                                                                                           396 LysThrAspSerileThrProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer
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                                                                                                                                                                                                                      1955 ACTCTATCAAAGATGCAGTACTCCTTGATATTGTTTACCCTGGTTATACG-----
                                                            GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly
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Sequence 3, Application US/10089678
Publication No. US20030017967A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, P
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
FILE REPERENCE: Q68821
CURRENT APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2002-05-02
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: PCT/JP01/06660
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
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    1510 AGATATGGCAATCTCCCTGTATTTGCTTGGACACATCGGAGTGCGGATGTTACAAATACA 1569
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                                                                                                                                                              ------TrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArg
                                  LeuGluProAspLysileThrGlnileAspAlaValLysGlyTrp-----GlyGly
                                                                                                                     GlySerSerHisIleValSerPhePheAspCysSerAsnSerSerGlyArgProSerAsn
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                                                                GTTTATTCAGATAAAATTACTCAGATACCAGTTGTAAAGGCACATACTTTAGTTTCAGGT
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                             100 CAGGIGACACGTACCGCCCAATACTCGGATTATTGTGTAAAGGTGGTATAACACTGGCTTA 759
                                                                                                                                                                                                                                                                                                         AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
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                                                                                                             LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla
                                                                                                                                    580 CCATTATTATCAGTGTATGCACAAGCAGCAATTTACATTTGCTATTATATACGAGATGCT
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                                                                               GCTTTAGAGCTTGATTTTGTTGCTAAAATCCCATCTTTTGCAATATCTGGACAGGAAGTA
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atatgaaaitctagatgcttcatcatctacttctgta	SerbsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr ::: TCCGATAATTCTGTTAGATACCTTTTAGCAAACGATCAAACGACACATTACAAAACAT	enTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPhelleGlyAsplle		ProGluAlaAlaLeuSerVa		AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly		TITIATAGITICATIGICAATIATGGCCATCAAGTACCGGGGGGAAATG	LeumetvalLeuvalGluGluLeuIeLysEysSerIleAspGlnArgValArgGluAsn	CTAATTGATCAAAAATAACAGATTCTGTAAGG	AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 		AlaTrpLeuValAenLysAenAspAepAepAspArgArgAlaLeuValThrGlnTyrAla 		1.EVRIATABDABRIPRESILLLYBABRINSELFTOLYBFRELYBGILLATGABRIPREGILLI.LE ::::: GCTTTAGAGCTTGATTTTGTTGCTAAAATCCCATTTTTGCAATATCTGGACAAGTA	LeuLeuLeuProvalTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla		GlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg			CAGGTGACACGTACCGCCCAATACTCGGATTATTGTGTAAAGTGGTATAACACTGGCTTA	AsnG]nPheAsnàraSerAsnà]aG]nAsnTrnVa]SerPheAsnàraBheAraThràsn						GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe		ThralaMetGluasnasnalaArgArgArgProSerTyrThrThrTrpLeuAsnArgIle	TCAGAAGTCGAAAGCGCTGTAATTCGTTCACCACACCTATTTGATATACTCAGTGAAATA	PheValtyrThrargThrLeuGlyAsnMetSerAspValargAsnIleTrp
AGTCCAA	SerAsnCy ::: TCCGATAR	AsnTyrLy	AACTATAA	SerThrTy	GAGACGTTTATTAGT	AsnSerVa	1101100	TTTTATAG	LeuMetVa	ATTATGA	AlaLeuAr	ececi-re	AlaTrple	maileach	GCTTTAGA	LeuLeuLe	 CCATTATI	AspTyrPh	TCCATITI	LeuGlnG	CAGGTGAC	AsnGlnPh	GATAAATT	MetThrie	ATGACATI	ProLeuAl	CCAATCGA	GlyValLe	AGAGAA	ThrAlaMe	TCAGAAGI	Phevalty GAATTTTA
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098 TACTCGGATAGCTTAACGGTAGGTGCAGATTCTTTTGCTTCAGGAGAGAAGTTTATGTA 2157
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                                                                                                                                                                      415 SerIleGluSerLeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsnAsnTyrIleThr 434
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                                                                                GlyLysThrAspSerIleThrProileGlnTyrPheAsnPheAlaAsnLeuSerValPhe
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GGTCATCAAATAAGCTACCATCGTGTCAGTAGGGGTAGTAATCTTCAACAAATGTATGGA 1164
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      IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle
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                                                                                                                     AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg
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APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Nicholas B. Duck
APPLICANT: Nicholas B. Duck
APPLICANT: Rainag Beng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn B. Sime
ITILE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
ITILE OF INVENTION: Peeticidal Activity Against Coleopterans
FILE REPERBENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT APPLICATION NUMBER: 60/242,838
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2003
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Mismatches:
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ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2001)
NAME/KEY: misc feature
NAME/KEY: misc feature
COCATION: (0)...(0)
OCHER INFORMATION: 1218-1
US-10-032-717-5
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Query Match:
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Pred. No.:
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163 GAATACCCTGGTTCACCTGAAGTACTTGTTAGCGGACAAGATGCAGCTAAGGCCGCAATT 222
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|ATCCTGGATAGTTTATTTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTA 582
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GATATAGTAGTAGTATCAGGTTTTAGGGGTCCCATTTGTTGGGCCCGATAGTGAGT
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                                                                               IlelleSerArgLeulleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla
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                                                               SerTyrLygAgnLygAgnGluTyrGluMetLeuAgpAlaLeuArglleAgnSerAgnMet
                                                                                                                                                                                                                                                    63 Thriyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle
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                                US-10-782-096-2 (1-682) x US-10-414-637-5 (1-2003)
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                                                            IleGlyPheValile------ProGlyProThrGlyAsnLeuValLysVal 558
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APPLICANT: Nicholas B. Duck
APPLICANT: Niang Peng
APPLICANT: Nonald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Simë
TITLE OF INVENTION: Genés Encoding No. US20030177528Alel Proteins With
TITLE OF INVENTION: Peqiticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/414,637
CURRENT PILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SQFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn 662
AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn
                                                                                                                        SerAspSerTrpHisSerLeuLysVal-------GlnAlaProGln
                                                                                                                                                                                                                                                  592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer
                                                                                                                                                                                    572 ArgGlnThrSerTyrArglleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla
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Conservative:
Mismatches:
Indels:
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Publication No. US20030177528A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
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OTHER INFORMATION: 1218-1
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FEATURE:
NAME/KEY: misc feature
LOCATION: (0)...(0)
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NAME/KEY: CDS
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AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuMetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10032717
Publication No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Xiang Feng
APPLICANT: Xiang Feng
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
TITLE OF INVENTION: Genes Encoding No. US20020151709A1e1 Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
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LOCATION: (1)...(2010)
OTHER INFORMATION: Maize optimized Cry1218-1
LOCATION: (0)...(0)
LOCATION: (0)...(0)
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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US-10-032-717-9
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                                                                                                                                     GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
                                                                                                                                                                                                                  LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
                                                                                                                                                                                                                                                                                           416 IleGluSer-------LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
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                                                           PheValTyrThr----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn 522
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APPLICANT: Ronald D. Flannagan

APPLICANT: Rafael Herrmann

APPLICANT: Theodore W. Kahn

APPLICANT: Theodore W. Kahn

APPLICANT: Theodore W. Kahn

APPLICANT: James K. Presnail

APPLICANT: James K. Presnail

APPLICANT: James K. Presnail

APPLICANT: Gao-Guo Yu

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

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FILE REFERENCE: 35718/287809

CURRENT APPLICATION NUMBER: 60/131, 786

PRIOR PILING DATE: 2003-06-05

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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cgn2 1/USPTO_epool/US10782096/runat_20012006_095216_24440/app_query.fasta 1.839
-Q=/Cgn2 1/USPTO_epool/US10782096/runat_20012006_095216_24440/app_query.fasta 1.839
-Q=/Cgn2 1/USPTO_epool/US10782096/runat_and -SUPPIX=blosum62
-LOOPCLE0 -LOOPEXT=0 -UNITS=bite -STRAT=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOOALIGN=200 -THR SCORE=pct -THR MAXE=100
-TTRANS=human40.cdi -LIST=45 -DOOALIGN=200 -NORM=ext -HEAPSIZE=500 -NINLEN=0
-MAXIEN=2.000000000 -USER=US10782096 @CGN 1 1 121 @runat 2001206_095216_2440
-NCPUS= -LOOP MAAD -NGG SCORES=0 -WAIT -DSPBLOCK=100 -DEV TINEOUT=120
-WARN TIMEOUT=30 -THERADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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988 GGAGTGATAGAATCATCCGTTATTCGACCCCCATGTATTTGATTATATAACGGGACTC 1047
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1165 ACTAATCAAAATCTACACACCACTAGTACCTTTGATTTTACGAATTATGATATTACAAG 1224
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AATAGAAGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCTAGCATTAGAA 1722
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---TATATATTT-----TTTGGAATGCCAGAAGTCGAGTTTTTCATGGTAAACCAATTG
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                                          299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr
                                                                                        319 GlyvalLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThe
                                                                                                                                                                                                                       359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly
                                                                                                                                                                                                                                                                     GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly
                                                                                                                                                                                                                                                                                            1105 GGTCATCAAATAAGCTACCATCGTGTCAGTAGGGGGTAGTAATCTTCAACAAATGTATGGA
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   GCAAAATTAAAAGGCACGAGCGCTAAACAATGGGTTGACTATAACCAATTCCGTAGAGAA
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GATATAGTAGGTAAATTACTATCAGGTTTAGGGGTCCCATTTGTTGGCCCGATAGTGAGT
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; FEATURE:
; NAWE/KEY: CDS
; LOCATION: (1)...(3621)
; FEATURE:
; NAWE/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry1218-1
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988 GGACTGATAGAATCATCCGTTATTCGACCACCCCATGTATTTGATTATATAAACGGGACTC 1047
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TCCAATGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAAATGCGCTACAAAATATG 120
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AGTCCAAATAATCAAAATGAATATGAAATTATAGATGCGACACCT---TCTACTTCTGTA
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                 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly
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APPLICANT: Ronald D. Flannagan
APPLICANT: Refael Herrmann
APPLICANT: Refael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: James K. Présnail
APPLICANT: James K. Présnail
APPLICANT: Cac-Guo Nu
APPLICANT: Cac-Guo Nu
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ACTILIS OF INVENTION: Gane's Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REPERENCE: 35718/291049
CURRENT FILING DATE: 2002-04-18
FRIOR APPLICATION NUMBER: 60/450,787
PRIOR PILING DATE: 2003-04-04-04
PRIOR PELING DATE: 2003-04-04-04
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Mismatches:
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Matches:
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Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
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US-11-108-389-1
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Best Local Similarity:
Query Match:
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1495 ACCGGATTAGTACCT-----GTATTTTCTTGGACACATCGAAGTGCAGATTAAAC 1545
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                                                                                                                              1165 ACTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATTATGATATTACAAG 1224
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276 ---TATATATTT-----TTTGGAATGCCAGAAGTCGAGTTTTTCATGGTAAACCAATTG 1326
                                                                                                                                                                                                                                                                                                                                                                           |||||||
|327 AATAATACCAGAAAGACGTTAAAGTAT-------AATCCAGTTTCCAAAGATATT 1374
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1375 ATAGCGACTACAAGAATTCGGAATTAGAATTACCTCCAGAAACTTCAGATCAACCAAAT 1434
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                                                                                                                                                                       416 IleGluSer-------LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
                                                                                                                                                                                                                                                             431 AsnīyrileThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuSer------GluLeuProGlyLysAspLysProAsn 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
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                                                                                                                                                                                                                                                                                                                                                AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrile
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GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly
                                                                                 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer
                                                                                                                                                                                                                  1225 ACTCTATCAAAGGATGCAGTACTCCTTGATATTGTTTACCCTGGTTATACG-----
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851 GATTATAAAGATTATTAAAAATGTCT-------GCGGGAAATGCTAGT 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle
                                                                                                                                                                                                                                           TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT PILING DATE: 2005-06-15
PRIOR PILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR PILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4874
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Matches:
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OTHER INFORMATION: Genomic DNA 1218-1
Sequence 17, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
                                                                                                                                                       Albert L. Lu
Billy Fred McCutchen
James K. Presnail
James F.H. Wong
                                                              APPLICANT: Andre R. Abad
APPLICANT: Rotald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Janes K. Presnail
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
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Best Local Similarity:
Query Match:
DB:
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; PRIOR APPLICATION NUMBER: 10/606,320	2105 ATAGCGAGTACAAGAGATTCGGAATTAGAATTACCTCCAGAAACTTCAGATCAACCAAAT 2164	qq
PRIOR FILING DATE: 2002-06-26 ; PRIOR APPLICATION NUMBER: 60/460,787 ; PRIOR FILING DATE: 2003-04-04	470 LeuSerGluLeuProGlyLysAapLysProArgProAsn 482	È
CURRENT FILING DATE: 2005-04-18 FRIOR APPLICATION WINBER: 60/391,786 FILING PITTING DATE: 2002-66-26		. A
; IILE OF INVENTION: ACLIVILY ; FILE REFERENCE: 35718/291049 ; CTRRENT APPLICATION NUMBER: US/11/108.389	469	3 8
APPLICANT: Cac-Guo Yu TITLE OF INVENTION: Genes Encoding Proteins	431 AsnTyrileThrSerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnile 449 ::: ::: ::: :::	රි සි
; APPLICANT: Billy Fred McCutchen ; APPLICANT: James K. Presnail ; APPLICANT: James F.H. Wong	1955 ACTCTATCAAAGGATGCAGTACTCCTTGATATTGTTTACCCTGGTTATACG 2005	qq
APPLICANT: Albert L. Lu APPLICANT: Place T. Add.	416 IleGluSer	ò
APPLICANT: KONAIO D. FIRANAGAN APPLICANT: RAfael Herrmann APPLICANT: Theodore W. Kahn	1895 ACTAATCAAAATCTACAGCACTAGTACCTTTGATTTTACGAATTATGATATTTACAAG 1954	qq
; GENERAL INFORMATION: ; APPLICANT: BOATE R. BABA	396 LysThrAspSerlleThrProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415	ò
; Sequence 17, Application US/11108389 ; Publication No. US20050261188A1 ; Carbon, Tanconamica.	::: ::: :::	qq
RESULT 4 US-11-108-389-17	377 GlyhisThrLeu:ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395	ò
Db 2783 AAT 2785	TCAAC	QQ
Qy 682 Asn 682	359 PheValTyrThrArgThrLeuGlyAgnMetSerAgpValArqAgnIleTrpGly 376	ò
Db 2723 ACATATGAAGCGGAACAAGATTTAGAAGCAGCC	GGAGTGATAGAATCATCGGTTATTCGACCACCCCATGTATTTGATTATATAACGGGACTC	· 8
Qy 663 ThrPheProAsnGlnSerLeuGluLysArc	raAraProSerTvrThrThrTrnLeuAsnAralle	8
Db 2663 AATTCAACATTATCTGGTATAGTTTACGTTGAC	SIS GIYVALLEUGIUSEKGIYGIYATARGINKIYKPKOKRPIYKABNAFARAKATAKAFA	Š €
Qy 645ThrGlnSerPheGlyThrHisAlalleAsp		ପୁର (
Db 2603 ACATTAAATTTAGCAACAGATAGTTCGCTAGC	299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318	ò
2543		QQ
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSei		ે ઠે
Db 2498 GATATTGTATTGCATGTAAACGATGCTCAGATT	259 ABNGINFNEABHAIGGERABHAIGGINABDIFDVAISGEFNEABHAIGFNEAIGINIABD 278 :::::: ::: ::: ::: ::: ::: 1493 GCBABBHHABABAGCGAGAGAGAGABAGAGAGAAGAAGAAAAAAAAAA	S 6
Qy 592 IlePheValGluHisSerGlySerSerHisIle	CAAATGAAACTTACTGCAGAATATTCTGATCACTGTGTAAAGTGGTATGAAACTGGTTTA	<u>අ</u>
7	LeuGlnGlyLeuileArgGluTyrLygAspHisCyslleThrPheTyrAsnGlnGlyLeu	ò
DB 2393 AAI'AGAAGIACINSSTICTGIAGGAACCITATT	1373 TCAATTTTTGGAGAAGAATGGGGATGGTCAACAACTACTATTAATAACTATTATGATCGT 1432	qq
559	219 AspTyrPheGlyhlaGlnTrpGlnLeuGlyAspAspGlulleArgAspAspAspAsnTyrlleArg 238	È
2333	CCATTCCTTACTGTATATGCAATGGCAGCCAACCTTCATTTACTGTTATTAAAGGACGCG	q
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2276	179 IleVallAspAsnPhePhGJuLysAsnMetProLysPheLysGluArgAsnPhGJulle 198	දු ද
523 AsnAroLeuGluProAspLvs11	1193 GAATGGGAAGAAATCCAAATGGTTCAAGAGCCTTACGAGATGTGCGAAATCGATTTGAA 1252	ପ୍ଧ
Qy 503 SerGlyGlyIleValSerLeuLeuThrPheGly	160 AlarrpLeuValAsnLysAsnAspAspAsnArgArgAlaLeuValThrGlnTyrAla 178	È
2165	1133 GCGCTTTCGGAATTAGAAGGATTAGGTAATAATTACCAATTATATCTGCGCTTGAA 1192	2 음
Qy 483 AlaGlyAspPheSerHisArgLeuSerTyril		g 2

11yProThrGlyGlyAsnLeuVallysVal 558 ilytrpalanisthrSerMetAspArgAsn 522 leAspAlavaliysGlyTrpGlyGlyAsm 542 || || || || || || || || rTcCGGCCGTTAAATGTTGG---GATAAT 2332 TTCAG----- 2542 rgGluGlnGluValAsnAspLeuPheile 681
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CGAAGAAAGCAGTGAATGCCTTGTTTACG 2782 TTCTAGCTCGATATGGCCTAGCATTAGAA 2452 ATGCTACT------GATGCA 2497 CATTGAAACATAATTTAGGTGAAGACCCT 2662 BpLyaPheGluPheIleProLeuAsn--- 662 leserAenPheAepAlaArgArgSerSer 502 eValSerPhePheAspCysSerAsnSer 611 -----GlnAlaProGln 571 yralaCysLeuValThrHisGlyAspAla 591 rgTyrArg----- 644 s With Pesticidal

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1433 CAAATGAAACTTACTGCAGAATATTCTGATCACTGTGTAAAGTGGTATGAAACTGGTTTA 1492
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| 1673 AACGIGICCITCAAIIGGIICC------IGGIAIGAC---AAAGCACCIICTIIC 1717
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2105 ATAGCGAGTACAAGATTCGGAATTAGAATTACCTCCAGAAACTTCAGATCAACCAAAT 2164
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                                              319 GlyvalLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe
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---TTTGGAATGCCAGAAGTCGAGTTTTTCATGGTAAACCAATTG
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                             AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp
                                                                                     Met Thr Leu Thr Val Leu Asp Leu Ala I le Leu Phe Pro Asn Tyr Asp Pro Arg Arg Tyr
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Matches:
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4874
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; OTHER INFORMATION: Genomic DNA 1218-1
US-11-108-389-17
                                                                    TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc_feature
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                                                                                                              4 TCCCCAACAACAACCAGAACGAGATCATCGACGCACCCC---TCCACCTCCGTG
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                                                                        SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet
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          US-10-782-096-2 (1-682)
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                                                   2498 GATATICIATIGCATGTAAACGATGCTCAGATTCAG------ATGCCAAAA 2542
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                                                                                                                                      SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrlleAspValProGly
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592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer
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GENERAL INFORMATION:
GENERAL ADDAG
APPLICANT: Radae R. Abad
APPLICANT: Refael Herrmann
APPLICANT: Refael Herrmann
APPLICANT: Albert L. Li
APPLICANT: Tabert L. Li
APPLICANT: Dames K. Presnail
APPLICANT: Gao-Guo Yu
APPLICANT: Cao-Guo Yu
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APPLICANT: APPLICATION NUMBER: 60/400,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR PILING DATE: 2003;04-04
PRIOR FILING DATE: 2003;04-04
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Publication No. US20050261483A1
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                           GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Randre B. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: James K. Presnail
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: Gac-Guo Yu
APPLICANT: Gac-Guo Yu
ITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
ITLE OF INVENTION: Activity
ITLE OF INVENTION: Activity
TITLE OF INVENTION: Activity
FILE REPRENCE: 35718/2981809
CURRENT APPLICATION NUMBER: 60/40,31786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-06-25
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SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: 1218-1A
US-11-058-727-11
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NAME/KEY: misc_feature
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1327 AACAACACCGGAAGACCCTCAAATAC------AACCCGGTGTCCAAGGACATC 1374
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                                                        1165 ACCAACCAGAAACCTCCACCTCCACCTTCGACTTCACCAACTACGACATCTACAAG 1224
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375 ATGGCCTCCACCGGGACTCCGAGCTCCGCCCCCCGGAGACCTCCGACCAGCCCAAC 1434
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GGCGTGATCGAGTCCTCCGTGATCCGCCCGCCGCACGTGTTCGACTACATCACGGCCTC 1047
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                                   359 PhevalTyrThr----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
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                                                                                                           GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly
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; Sequence 11, Application US/11058727

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Sequence 5, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Plannagan
APPLICANT: Rafael Herrmann
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1276 ---TATATATTT:-----TTTGGAATGCCAGAAGTCGAGTTTTTCATGGTAAACCAATTG 1326
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|327 AATAATACCAGAÀAGACGTTAÀAAGTAT------AATCCAGTTTCCAAAGATATT 1374
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1165 ACTAATCAAAATCTACACACACAGCACTAGTACCTTTGATTTTACGAATTATGATATTACAAG 1224
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1375 ATAGCGAGTACAÀGAGATTCGGAATTAGAATTACCTCCCAGAAACTTCAGATCAACCAAAT 1434
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                           140 AlakeuArgGlukeuGluGlykeuGlnGlyIleMetArgkeuTyrGlnThrArgkeuGln 159
                                                                                  160 AlaTrpLeuValAsnLysAsnAspAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
                                                                                                                                      179 ileValaspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
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343 TTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATAGCAGAATATGCAAGGAATAAA 402
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1495 ACCGGATTAGTACCT-----GTATTTTCTTGGACACATCGAAGTGCAGATTTAAAC 1545 ::: ||| 1663 AATAGAAGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCTAGCATTAGAA 1722 1768 GATATTGTATTGCATGTAAACGATGCTCAGATTCAG--------ATGCCAAAA 1812 1813 ACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCAGATGCTATCACA 1872 1723 AAAGCAGGGAAATATCGTGTAAGACTGAGATATGCTACT-------GATGCA 1767 1873 ACATTAAATTTAGCAACAGATAGTTCGCTAGCATTGAAACATAATTTAGGTGAAGACCCT 1932 543 IleGlyPheValIle------ProGlyProThrGlyGlyAsnLeuValLysVal 558 559 SerAspSerTrpHisSerLeuLysVal-------GlnAlaProGln 571 592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg--------644 1933 AATTCAACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCCAGTAGAT 1989 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn 662 523 AsnArgLeuGluProAspLysileThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn SerglyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrlleAspValProGly AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer APPLICANT: Malage Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: James R. Presnail
APPLICANT: Gao-Guo Yu
ITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
ITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR PILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-06-25
NUMBER OF SED ID NOS: 134
SOSTWARE FESTSEQ for Windows Version 4.0

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1327 AACAACACCCGCAAGACCTCAAATAC------AACCCCGTGTCCAAGGACATC 1374
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; LOCATION: (1)...(2010)
; OTHER INFORMATION: Maize optimized Cry1218-1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
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                                                                 160 AlaTrpLeuValAsnLysAsnAspAspAsnArg---ArgAlaLeuValThrGlnTyrAla
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                      SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Theedore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT APPLICATION NUMBER: 60/491,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
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ORGANISM: Bacillus thuringiensis (truncated)
PEATURE:
NAME/KEY: CDS
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Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: 1218-1A
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Pred. No.:
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CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 49
FILE REFERENCE: 35718/287809
                                                                                                                                                                                        FEATURE:
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---TITGGAATGCCAGAAGTCGAGTTTTTCATGGTAAACCAATTG 1326
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1603 TTACCGITIGITCCAGIGGIAAAAGGACCAGGACAIACAGGAGGGGATITAITACAGIAI 1662
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1375 ATAGCGAGTACAAGAGTTCGGAATTAGAATTACCTCCAGAACTTCAGATCAACCAAAT 1434
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             -----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
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                                   1225 ACTCTATCAAAGGATGCAGTACTCCTTGATATTGTTTACCCTGGTTATACG-----
                                                            AsnīyrileThrSerGlnTyrGlyValSerArgVal ---IlePheAsnThrSerAsnIle
                                                                                                             AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle
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ORGANISM: Bacillus thuringiensis (mutated)

LENGTH: 2022

TYPE: DNA

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APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: James K. Preenail
APPLICANT: James R. Preenail
APPLICANT: James R. Preenail
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
                                                     Sequence 49, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
RESULT 9
US-11-058-727-49
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173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AlabeuArgGlubeuGluGlybeuGlnGlylleMetArgbeuTyrGlnThrArgbeuGln 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 GCGCTTTCGGAATTAGAAGGATTAGGTAATTATCCAATTATATCTAACTGCGCTTGAA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522
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                                                                                                                                                                                                          SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet
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243
119
259
85
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Mismatches:
Indels:
                                                                                                                                                                              US-10-782-096-2 (1-682) x US-11-058-727-49 (1-2022)
                                                                         Length:
Matches:
                                                                      7.6e-100
925.50
51.3%
34.4%
25.7%
             ... (2022)
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Best Local Similarity:
; NAME/KEY: CDS
; LOCATION: (1)
US-11-058-727-49
                                                           Alignment Scores:
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1927 CATAATGTAGGTGAAGACCCTAATTCAACATTATCTGGTATAGTTTACGTTGACGAATC 1986
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1663 GATTTATTACAGTATAGAAGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATAT 1722
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                                                                                                                 -----ATGCCAAAAACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTAAAGTT
                                                                                                                                                                                                                                                     643 Tyr------ArgThrGlnSerPheGlyThrHiBAlaIleAgpLyBPhe
                                                              607 AspCysSerAsnSerSerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyr
                                                                                                                                                                                                    627 IleAspValProGlyllePheThrProSerlle------AsnProLeulleArg
                                                                                                ThrHisGlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPhePhe
554 AsnLeuValLysValSerAspSerTrpHisSerLeuLysVal---
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Best Local Similarity:
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          314 ProvalGlyPheThrGlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnPro 333
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                                                                                                              TyrAsnGlnGlyLeuAsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsn 273
                                                                                                                             274 ArgPheArgThrAspMetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyr 293
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US-11-026-727-81

Sequence 81, Application US/11058727

Publication No. US20050261483A1

SERNERAL INFORMATION:

APPLICANT: Andre R. Abad

APPLICANT: Rafael Herrmann

APPLICANT: Albert L. Lu

APPLICANT: Albert L. Lu

APPLICANT: Albert L. Lu

APPLICANT: Albert L. Lu

APPLICANT: James R. Presnail

APPLICANT: James R. P. Wong

APPLICANT: James R. P. Wong

APPLICANT: James P. H. Wong

APPLICANT: Albert S. So-Guo Yu

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Activity

FILE REFERENCE: 35718/287809

CURRENT APPLICATION NUMBER: 05/40,737

CURRENT APPLICATION NUMBER: 60/460,737

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-05

PRIOR FILING DATE: 2003-04-05

PRIOR FILING DATE: 2003-04-05

PRIOR FILING DATE: 2003-04-05

PRIOR FILING DATE: 2003-04-05

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PRIOR FILING DATE: 2003-04-05

PRIOR FILING DATE: 2003-04-05

SOFTWARE: FREESEQ for Windows Version 4.0

SEC ID NO 81

TEMPLY DATE: 2003-04-04

SEC ID NO 81

TEMPLY DATE: 2003-04-04

SEC ID NO 81

TEMPLY DATE: 2003-04-04

SEC ID NO 81

TEMPLY DATE: 2003-04-04

PRIOR PARESEQ for Windows Version 4.0 2022 243 1119 259 85 Length: Matches: Conservative: Mismatches:

Oy 354 TrpLeuAsnArgilePheVallyrThr- ::::: Db 1048 TATATAACGGGACTCACAGTGTATACAC Oy 372 ArgAsnIleTrpGlyGlyHisThrLeu- Dh 1108 ACACAT		1225 426 1285	Qy 445 AsnThrSerAsnlleAsnAsnValProG 137 ATGGTAAACCAATTGAATAATACCAGAA Qy 465 ProSerGInThrIleLeuSer Db 1375 GTTTCCAAAGATATTATAGGGAGTACAA	Qy 478 LysProArgProAsnalaGlyAspPheS :: 1435 TCAGATCAACCAAATTATGAGTCATATA Qy 498 AlaArgArgSerSerSerGlyGlyIleV 1495 GCGACGGGTAACACTACCGGATTAGTAG	Oy 518 SerMetAspargAsnasnArgLeuGluP	554 1663 568 1723	Qy 587 ThrHisGlyAspAlailePheValGluH Db 1777GATGCAGATATTGTATTGC Qy 607 AspCysSerAsnSerSerGlyArgProS Db 1819ATGCCAAAAACAATGAACCCACACCACCACCACCACCACCACCACCACCACCAC	Qy 627 IleAspValProGlyIlePheThrProS bb 1873 GCAGATGCTACCAGTTA Qy 643 TyrArgThrG Db 1927 CATAATTTAGGTGAAGACCCTAATTCAA Qy 657 GluPhelleProLeuAsn 662 Qy 657 GluPhelleProLeuAsn 662 Db 1987 GAATTCATCCCAGTAGAT 2004 BESHILT 11	KESOTI II
3 SerTyrLyshanLyshanGlufyrGluMetLeuhspalaLeuArgIleAsnSerAsnMet 22	TCCAATGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAAATGCGCTACAAAATATG ABNTYZLYBG1uTrpLeuAsnMet CysAspSerAsnThrG1nPheIleG1yAspIleSer ::: :::::	93 INTIVESEFEROGIUALAGAIGANSENALAGABALAVAILEUTNIGLYILE 81 163 GAATACCTGGTTCACCTGAAGTACTTGTTAGCGGACAAGATGCAGCTAAGCCGCAATT 222 82 ASINSERVAIGLYTHILLEUSERASILEUGLYVALPTOLEUALASEGCINSERPHEGLY 101 223 GATATAGTAGGTAAATTACTATCAGGTTTAGGGGTCCCATTTGTTGGGCCGATAGTGAGT 282	102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAspProPheGluAla 119 ::: :::::		ValThrGlnTyrAle .::::: CGAAATCGATTTGAA ArgAsnPheGlulle ArgAshTTTTTTAAAATTTTTTAAAATTTTTTAAAATTTTTTAAAA	LeuleuhrgabalaaspTyrPheGlyalaGlnTroglnLeuGlyaspaspGluIleArg :: TATTAAAGGGGGGTCAATTTTGGGAAGGGGGGGGGGGG	254 TyrAsnGlnGlyLeuAsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsn 273	294 ASPProArgArgTyrProLeualaValLysThrGluLeuThrArgGluValTyrThrAsp 313	
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ACCT-----GTATTTTCTTGGACACATCGA 1545 OGlySerLeuArgTyrGluValProAlaAsnLeu 464 :::|||:::|||| AAAGACGTTAAAGTAT-----AATCCA 1374 AGAGATTCGGAATTAGAATTACCTCCAGAAACT 1434 UProAsplysileThrGinileAspAlaVallys 537 rccagtggtaaaaggaccaggacatacaggaggg 1662 |||::: |GGTTCTGTAGGAACCTTATTTCTAGCTCGATAT 1722 rTyrArgileArgLeuhrgTyrAlaCysLeuVal 586 |||| 3CATGTAAACGATGCTCAGATTCAG----- 1818 AGGTGAGGATCTGACATCTAAAACTTTTAAAGTT 1872 ::::::
RATITAGCAACAGATAGTITGGGTITGCAGTIAAA 1926 AACATTATCTGGTATAGTTTACGTTGACGGAATC 1986 ::: |||||| ::: AGCTACCATCGTGTAGGGGTAGTAATCTT 1164 u---ValGluAsnGlyAsnAspGlySerGluIle 390 rSerGlnTyrGlyValSerArgVal---IlePhe 444 ------GluLeuProGlyLysAsp 477 sserHisArgLeuSerTyrIleSerAsnPheAsp 497 oHisserLeuLysVal------567 SerIle------AsnProLeuIleArg 642 r-----ArgThrLeuGlyAsnMetSerAspVal 371 eValSerLeuLeuThrPheGlyTrpAlaHigThr 517 uhisSerGlySerSerHisileValSerPhePhe 606 SerAsnThrLeuLeuGluSerAspPheArgTyr 626 GlnSerPheGlyThrHisAlaIleAspLysPhe 656 lile-----ProglyProThrGlyGly 553

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988 AAAGCACCTTCTTTGGAGTGATAGAATCATCGTTATTGGACCACCCCATGTATTGAT 1047
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                                                                                                                           GAATGGGAAGAAATCCAAATGGTTCCCGGTTTCGAAGTCGACAAGCCTTACGAGATGTG 522
                                                                                                                                                                                                                                                                                               583 ACAAATTTTGAAGTACCATTCCTTACTGTATATGCAATGGCAGCCAACCTTCATTTACTG 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 ArgPheArgThrAspMetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyr 293
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140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln
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TIATTAAAGGACGCGTCAATTTTTGGAGAAGAAGAAGGATGGTCAACAACTACTATTAAT
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                                          AlaTrpLeuValAsnLysAsnAspAsp------AsnArgArgAlaLeu-----
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           Sequence 49, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Theedore W. Kahn
APPLICANT: Theedore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: James F.H. Wong
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APPLICANT: James F.H. Wong
APPLICANTION NUMBER: 105/1/108,389
CURRENT FILING DATE: 2002-04-18
FRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-06-25
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ORGANISM: Bacillus thuringiensis (mutated)
PEATURE:
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TCAGATCAAATTATGAGTCATATAGCCATAGATTATGTCATATCACAAGTATTCCC 1494
                                                                                                                                                                                                                                                                                    587 ThrHisGlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPhePhe 606
                                                                                                                                                                                                                                                                                                                                     607 AspCysSerAsnSerSerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgfyr 626
                                                                                  SerMetAspArgAsnAsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLys
                                                                                                                                                                                                                                                                                                                                                                                                   AlaArgArgSerSerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThr
                                                             GCGACGGGTAACACTACCGGATTAGTACCT-----GTATTTTCTTGGACACATCGA
                                                                                                                                                                                                                                                           1723 GGCCTAGCATTAGAAAAGCAGGGAAATATCGTGTAAGACTGAGATATGCTACT-----
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                                                                                                                                    GlyTrpGlyGlyAsnIleGlyPheValIle------ProGlyProThrGlyGly
                                                                                                                                                                                   AsnLeuValLysValSerAspSerTrpHisSerLeuLysVal-------
                                                                                                                                                                                                                                    ---GlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuVal
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APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Bally Fred McCutchen
APPLICANT: James F. Presnail
APPLICANT: Cac-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT FILING DATE: 2005-04-18
FRIOR PAPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 00/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-06-25
SOFTWARE PRESCO for Windows Version 4.0
SEQ ID NO 81
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 81, Application US/11108389 Publication No. US20650261188A1 GENERAL INFORMATION: APPLICANT: Andre R. Abad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ronald D. Flannagan
Rafael Herrmann
Theodore W. Kahn
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US-11-108-389-81
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TCCAATGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAAATGCGCTACAAAATATG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
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GATATAGTAGGTAAATTACTATCAGGTTTAGGGGTCCCATTTGTTGGGCCGATAGTGGT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 AlaTrpLeuValAsnLysAsnAspAsp------AsnArgArgAlaLeu----- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 ValThrGlnTyrAlaileValAspAsnPhePheGluLysAsnMetProLysPheLysGlu 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAsnCysTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
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AGTCCAAATAATCAAAATGAATATGAAATTATAGATGCGACACCT---TCTACTTCTGTA
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121 GATTATAAAGATTATTTAAAAATGTCT----------GCGGGAAATGCTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAgpAlaValLeuThrGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuMetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 ArgAsnPheGluIleLeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIle
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243
1119
259
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ORGANISM: Bacillus thuringiensis (mutated)
                                                                                                                                                                           7.6e-100
925.50
51.3%
34.4%
                                                                        ... (2022)
                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                Percent Similarity:
                                             ; NAME/KEY: CDS
; LOCATION: (1)
US-11-108-389-81
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        -----ATGCCAAAAACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTT 1872
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                                                          627 IleAspValProGlyIlePheThrProSerIle------AsnProLeuIleArg
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| Sequence 7, Application US/11058727
| Publication No. US2005026148341
| SeBREAL INFORMATION:
| APPLICANT: Andre R. Abad
| APPLICANT: Theodore W. Kahn
| APPLICANT: Theodore W. Kahn
| APPLICANT: Theodore W. Kahn
| APPLICANT: Theodore W. Kahn
| APPLICANT: James F. F. Wong
| APPLICANT: James F. Wong
| APPLICANT: James F. Wong
| TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
| TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
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| TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
| TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
| TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
| TITLE OF INVENTION: 1000-16-26
| PRIOR FILING DATE: 2003-04-04
| PRIOR FILING DATE: 2003-06-25
| NUMBER OF SEQ ID NOS: 134
| COFTWARE FERSENCE FEAUSOR WINDOWS VERSION 4.0
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Matches:
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ORGANISM: Bacillus thuringiensis (mutated)
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1495 GCGACGGGTAACACTACCATAGTACCT-----GTATTTTCTTGGACACATGGA 1545
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                                                                                                                                                                                                                                                                                334 AsnAsnThrThrPheThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrThr 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 ArgAsnIleTrpGlyGlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIle 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 ThrHisAsnPheGlyLysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsn 410
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                                                                                AspProArgArgTyrProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAsp 313
                                                                                                                                                                                  314 ProvalGlyPheThrGlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnPro 333
                                                                                                                                                                                                                                  943 CCACTGGGCGCGGTAAACGTGTCTTCAATTGGTTCC-------TGGTATGAC--- 987
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SerMetAspArgAsnAsnArgLeuGluProAspLys1leThrGlnIleAspAlaValLys
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1327 GTAAACCAATTGAATAACCAGAAAGACGTTAAAGTAT-------AATCCAGTT 1374
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763 GAAACTGGTTTAGCAAAATTAAAAGGCACGAGGCGCTAAAACAATGGGTTGACTATAAAACCAA
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                                                                                                                        LeuArgAspAlaAspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAsp
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|63 GAATACCCTGGTTCACCTGAAGTACTTGTTAGCGGACAAGATGCAGCTAAGGCCGCAATT 222
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|TCCAATGATTCTÀACAGATACCCTTTTGCGAATGAGCCAACAAATGCGCTACAAAATATG 120
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APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/297809
CURRENT APPLICATION NUMBER: 050-02-15
PRIOR APPLICATION NUMBER: 06/391,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 2022
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239
116
268
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Mismatches:
Indels:
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Matches:
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Query Match:
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LOCATION: (1)
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US-11-058-727-25
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Mismatches:
Indels:
                                                    US-10-782-096-2 (1-682) x US-11-058-727-29 (1-2022)
 34.0%
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  Similarity:
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                                                                                                                      568 GlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThr 587
                                                                                                                                                                           588 HisGlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPhePheAsp 607
                                                                                                                                                                                                                                                                                   AspValProGlyIlePheThrProSerIleAsnProLeuIleArgTyrArg-----
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Matches:
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               TrpGlyGlyAsnIleGlyPheValIle---
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Publication No. US20050261483A1
GENERAL INFORMATION:
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APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
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335 988	ABITHLTHLPHETHLAIAMEtGluABINABANAGARGARGPROSERTYTHLTHLTLP 354 GCACCTICITICGCAGIGATAGAATCATCGTTATTCGACCACCCAIGIATTTGATAT 1047
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412	ServalpheSerlieGluSer
427	ThrGlualaasnasnatrileThrSerGlnTyrGlyValSerArgValIlePheasn 445
446	ThrSerAbnileabanasnValProGlySerLeuArgTyrGluValProAlaabnLeuPro 465
466 1375	SerGlnThrIleLeuSer
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519	MetaspargasnasnargLeugluProasplyslleThrGlnileaspalaVallysGly 538 :::
539	TrpGlyGlyAsnijleGlyPheVallleProGlyProThrGlyGs 554
555	LeuvallysvalšeraspSerTrpHisSerLeulysval
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628 1873	AspvalProGlyilePheThrProSerIleAsnProLeuIleArgTyrArg 644 GATGCTATCACAACATTAAATTTAGCAACAGATAGTTCGCTAGCAGTGAAACATAATGTA 1932
645 1933	ThrGlnSerPheGlyThrHisAlalleAspLysPheGluPheIle 659 ::: GGTGAAGACCCTÄATTCAACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATC 1992

Qy 660 ProLeuAsn 662 |||::::: Db 1993 CCAGTAGAT 2001

Search completed: January 21, 2006, 04:28:55 Job time : 366 secs

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Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carozzi,N., Hargiss,T., Koziel,M.G., Duck,N.B. and Carr,B. Delta-endotoxin genes and methods for their use Patent: WO 2004074462-A 19 02-SEP-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bacillus thuringlensis"
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Sequence 19 from Patent WO2004074462.
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                                                                                              January 20, 2006, 22:28:18; Search time 9149 Seconds (without alignments) 4146.672 Million cell updates/sec
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               version 5.1.7
- 2006 Biocceleration Ltd.
                                                                 nucleic search, using frame plus p2n model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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120 120 360 480 180 180 240 100 300 140 420 160 540 200 900 80 20 9 40 9 AATATGTCTAAATTGTTATCCAAGGTATCCACTAGCAAAAGATCCACAAATGACTATGCGA IleAsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPhe MetValLeuValGluGluLeuIleLysEysSerIleAspGlnArgValArgGluAsnAla LeudrgGluLeuGluGlyLeuGluGlyIleMetArgLeufyrGlnThrArgLeuGlnAla AspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeu GATAACTITITICGAAAAGAATATGCCAAAATTCAAGGAAAGAAAGTTTGAAATTTATTG AsnMetSerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArg AsnThrAsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAsp | IleSerThrTyrSerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGly ATAAGCACGTATTCTAGCCCTGAAGCTGCTTTAAGTGTACGAGATGCTGTTTTAACGGGT ATTAACAGTGTAGGGACTATACTTTCGAATTTAGGGGTCCCTTTGGCAAGTCAATTT TrpLeuValAsnLysAsnAspAsnArgArgAlaLeuValThrGlnTyrAlaIleVal 2049 682 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: (1-2049)x CQ868318 1.9e-259 3597.00 100.0% 100.0% US-10-782-096-2 (1-682) Percent Similarity: Best Local Similarity: Alignment Scores: 21 41 121 61 181 81 101 301 361 61 241 121 141 161 481 421 181 541 Query Match: DB: .. No.: ORIGIN 셤 셤 g ઠે 셤 g 8 & a g 셤 ò a ઠે ઠે ò ઠે ℰ ઠે ઠે ઠે

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LeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAlaAspTyr TTACCAGTATATGCACAAGCCGCGAATTTGCATTTAATTTTATTAAGAGATGCTGATTAT

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1861 GAGAGTGATTTTCGCTATATTGATGTTCCAGGTATTTTTACACCATCATAAATCCCTTA
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               1141 CATAACTTTGGTAAAACTGATTCTATTACTCCTATTCAATATTTTAATTTTGGCGAACCTT
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                                                                    GluLeuProGlyLygAspLysProArgProAsnAlaGlyAspPheSerHisArgLeuSer
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HisAsnPheGlyLysThrAspSerIleThrProlleGlnTyrPheAsnPheAlaAsnLeu
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/ LEGARGAE TEACH TO = "MSPRONDEYELIDATBSTSVSNDSNRYPPANEPTNALQNMDYKD
YLKMSAGNASEY BGSPEVLVSGQDAAKAA LDIVGKLLSGLGVPFVGFIVSLYTOLIDI
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LASTSTPDFTNYDIYTKTLSGTSARYIRHWAGHOISYHRVSRGSNLQQMYGTNON
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ARYGLALEKAGKYRVLRYATDADIYLHVNDAQIQMPKTWAPGEDLTSKTFKVADAIT
TANLATDSSLALKARLGEDPNSTLSGIYVVORIBFIPVDETYBRYKRARGARKANNAL
FINNTROGLRFGYTDYRWOANLVGCLSDDLYPNERKLLEPDANEARKLSBANLLQD
PDPQEINGENGWTASTGIEVIERHQTNRIVKNVPDDLLPDNVSPVSINRCSBQK
YVNSRLEVENRSGEAHEFSIFTIHHQTNRIVKNVPDDLLPDVSPVNSDGSINRCSBQK
YVNSRLEVENRSGEAHEFSIFTIHHQTNRIVKNVPDDLLPDVSFYTTDPEGYATLGNLELVEE
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IleValSerPhePheAspCysSerAsnSerSerGlyArgProSerAsnThrLeuLeuGlu
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                                                 TyralaCysteuValThrHisGlyAspAlaIlePheValGluHisSerGlySerSerHis
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/ organism="Bacillus thuringiensis"

/ mol type="unassigned DNA"

/ db_xref="taxon:1428"

/ note="cry1218-1"

1. 3621

/ note="unnamed protein product"

/ codon start=1

/ transl_table=11

/ protein_id="CAJ21051.1"

/ db_xref="G1:77793184"
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                                                                          GGAGCACAGTGGCAATTAGGTGATGATGAAATTCGTGATAATTATATCGAGACTACAAGGA
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GPLSGDALERLQREEQQWKIQWTRRREETDRRYMASKQAVDRLYADYQDQQLNPDVEI TDLTAAQDLIQSIPYYYNEMFPEIPGMNYTKFTELTDRLQQAWSLYDQRNAIPNGDFR NGLSWWNATFGYEVQQINHTSYLVIPWDEQYSQQFTVQPNQRYYLRYTARKEGYGNG YVSIRDGGNQTETLTFSASDYDTNGWYNTQVSNTNGYNTNNAYNTQASSTNGYNANNW YNTQASNTNGYNTNSYYNDQTGYITKTVTFIPYTDQMWIEMSETEGTFYIESVELIV VE." 402 218 642 238 702 258 762 822 ||||||| TCCAATGATTCTAACAGATACCCTTTTGGGAATGAGCCAAAAATGCGCTACAAAATATG 120 AlaTrpLeuValAsnLysAsnAspAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178 81 9 42 62 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln LeuMetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn |||| |TTTATGGAACAAGTAGAAGAACTCATTAATCAAAAAATAGCAGAATATGCAAGGAATÁAA GCGCTTTCGGAATTAGAAGGATTAGGTAATAATTACCAATTATATCTAACTGCGCTTGAA |||:::||||:::|||||::: ATCCTGGATAGTTTATTTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTA CCATICCITACIGIATATGCAATGGCAGCCAACCITCAITIACIGITAITAAAGGACGCG SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet SerAsnCysTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer ---GCGGGAAATGCTAGT ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlylle AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPhedly ::: |||||| ::: ||||||| GATATAGTAGTTAGGGGTCCCATTTGTTGGGCCGATAGTGAGT IlelleSerArgLeulleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle LeuLeuLeuProValTyrAlaGlnAlaAlaAgnLeuHisLeuIleuArgAspAla AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg TCAATTTTTGGAGAAGAATGGGGATGGTCAACAACTACTATTAATAACTATTATGATCGT LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 3621 248 1119 276 25 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: :::|||||||::::::||| GATTATAAAGATTATTTAAAAATGTCT----(1-3621)x CS130946 5.86e-61 948.00 50.9% 34.4% 26.4% US-10-782-096-2 (1-682) Percent Similarity: Best Local Similarity: Scores: 63 102 343 463 259 23 43 121 163 82 283 120 140 160 523 199 219 239 19 403 179 583 643 703 763 223 Match: No.: Ignment ORIGIN Best L Query DB:

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||||||| ---TATATATTT-----TTTGGAATGCCAGAAGTCGAGTTTTTCATGGTAAACCAATTG 1326 1374 ::: ||||||| |::|||||| |:::|||||:::::: THACCGTTTCTTCAGTGGTATACAGTACAGGAGGGGATTTATTACAGTAT 1662 GATATTGTATTGCATGTAAACGATGCTCAGATTCAG--------ATGCCAAAA 1812 GARGIGATAGAATCATCCGTTATTCGACCACCCATGTATTTGATTATATAACGGGACTC 1047 1164 1434 AATACAATATTCAGATAAATCACTCAAATTCCGGCCGTTAAATGTTGG---GATAAT 1602 338 395 430 449 469 502 542 942 987 358 376 591 GlyvalLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr |||::: |CCAATGGAAACGAAAGCACAACTAACAAGGGAAGTATATACAGATCCACTGGGGGGTA AACGIGICTICAATIGGIICC------IGGIAIGAC---AAAGCACCIICIIIC ThralaMetGluAsnAsnAlaArgArgArgProSerTyrThrTrpLeuAsnArgIle PheValTyrThr----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrlle |||||||| | AATAATACCAGAAAGACGTTAAAGTAT------AATCCAGTTTCCAAAGATATT |||||||| ::: ||||||| || ATAGCGAGTACAGAATTAGAATTACTCCAGAAACTTCAGATCAAAT AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer TATGAGTCATATAGCCATAGATTATGTCATATCACAAGTATTCCCGGGGGGTAACACT SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn lleGlyPheVallle------ProGlyProThrGlyGlyAsnLeuValLysVal MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr AsnīyrileThrSerGlnTyrGlyValSerArgVal --- IlePheAsnThrSerAsnIle LeuSer-------GluleuProGlyLyBAspLysProAsn -GlnAlaProGln ArgGlnThrSerTyrArg1leArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer lyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer actetațeaaggatgeagtactecrigatattetriaecergerraraeg -:: AAAGCAGGGAAATATCGTGTAAGACTGAGATATGCTACT-SerAspSerTrpHisSerLeuLysVal---ថ 1048 1105 1225 431 470 1375 1663 1723 377 1276 1327 483 1495 823 299 883 319 943 339 988 359 396 416 450 1435 503 523 543 1603 279 1546 559 572 8 8 8 원 장 a ઠે 셤 ò 원 상 원 8 6 8 6 6 B 6 B 6 B 6 ያ ያ a à 셤 g g 셤 a ò 8 જે à

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0y 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrlleAspValProGly 631 1813 ACAATGAACCCAGGTGAGGATCTGACATCTTAAAGTTGCAGATGCTATCACA 1872 0y 632 IlePheThrProSerIleAsnProLeulleArgTyrArg	AUTHORS AUTHORS AUTHORS AUTHORS Plant activation of insect toxin JOURNAL Patent: Wo 2005063996-A 514-301-2005, JOURNAL Patent: Wo 2005063996-A 514-301-2005, Batent: Wo 2005063996-A 514-301-2005, International Inc. (US) Authors

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LAVLDVVALEPNYDTRYTYPREGTKAQLTREVYTDPLGANNVSSIGSWYDRAFSEGVI ES
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SVIRPHYPEVYTGLTVYTOSRSI SSARY I RHWAGHQI SYTHRYSRGSNLOQWYGTNON
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YNDVSKDI I ASTROYSELLEPPETSDOPNYESSYSHRLCHITSI PATGWTTGLVEVFSWT
HRSADLNNTI YSDKI TQI PAVKOMULP FVPVVKGPGHTGGDLLQYNRSTGSVGLFL
ARVCLALERAGKYRYRLKATDADI LHVNDAQI QMPKTWNFGEDLTSKTFKVADAI T
TLNLATDSSLALKHNLGEDPNSTLSGI VYVDR I EFI PVDETYBARGLISAAKKANDAL
FTNNTGGLRRQYTYRYRLANGYANDADI CHONGTYBARGLISAAKKANDAL
PDFQBI NGENGWTASTGI EFI FRHQTNR I VKNV PDDLLEPDVSPVNSDGSI INRCSBQK
KPYNRYRLRGGRAHFFSI PI DTGEI DYNRNI YKNV PDDLLEPDVSFYTLGGLEVET
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TDLTAAQDLIOSIPYVYNEMFPEIPGMNYTKFTELTDRLOQAWSLYDORNAIPNGDFR
NGLSNWNATPGVEVOLINHTSVLVIENWDEOVSOOFTVOPNORYVLRYTARKEGVGNG
YVSIRDGGNOTETLIFSASDYDTNGMYNTQVSNTNGYNTNNAYNTQASSTNGYNANNM
XNTQASNTNGYNTNSVYNDQTGYITKTVTFIPYTDQMWIEMSETEGTFYIESVELIV
VE"
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Matches:
Conservative:
Mismatches:
Indels:
PONT DE NEMOURS AND COMPANY (US)
                                                                                                                                                                      note="unnamed protein product"
                                                                               /mol_type="unassigned DNA"
/db_xref="taxon:1428"
/note="Cry1218-1"
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                                                              organism="Bacillus"
                   Location/Qualifiers
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AAAGCAGGGAAATATCGTGTAAGACTGAGATATGCTACT------GATGCA 1767
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1873 ACATTAAATTTAGCAACAGATAGTTCGCTAGCATTGAAACATAATTTAGGTGAAGACCCT 1932
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, Bacillus
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                          AATACAATATTCAGATAAATCACTCAAATTCCGGCCGTTAAATGTTGG----GATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                   543 IleGlyPheVallle------ProGlyProThrGlyGlyAsnLeuValLysVal
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Genes encoding novel proteins with pesticidal activity against
  AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrile
                                                                                    -----GluLeuProGlyLysAspLysProArgProAsn
                                                                                                                                                                        AladlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer
                                                                                                                                                                                                                                                          SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn
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Patent: WO 0234774-A 1 02-MAY-2002;
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Sequence 1 from Patent W00234774
AX543924
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                                                     160 AlaTrpLeuValAgnLysAgnAspAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
                                                                                         IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
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                  AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln
                                                                  583 CCATTCCTTACTGTATATGCAATGGCAGCCAACCTTCATTTACTGTTATAAAGGACGCG
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                                   TATGAGTCATATAGCCATAGATTATGTCATATCACAAGTATTCCCGCGACGGGTAACACT
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TTACCGTTTGTTCCAGTGGTAAAAGGACCAGGACATAACAGGAGAGAGGGATTTATTACAGTAT
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Patent: WO 2005066349-A 17 21-JUL-2005;
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| ACATATGAAGCGGAACAAGATTTAGAAGCAGCGAAGAAGCAGTGAATGCCTTGTTTACG
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                                                          ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle
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                                                                                                                                                                                                                                                                                                                                   Genes encoding novel proteins with pesticidal activity against
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Sims,L.E.
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Bacillus thuringiensis
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus;
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Patent: WO 0234774-A 27 02-MAY-2002;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
Location/Qualifiers
1. .48/74
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AARRPPHYDRYTGLTVYTKRSFTSDRYMRYMAGOLGISKHTGTSSFFTGMYGTNQN
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INGENGWTASTGIEVIEGDAYFKGRYLRLPGAREIDTETYPTYLYQYVBEGYLKPYTR
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WIEISETEGTFYIESSVELIVDVE"
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TCCAATGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAAATGCGCTACAAATATG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 IlelleSerArgieuileGlyileLeuTrpAlaGly-----ProAspProPheGluAla
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                                          organism="Bacillus thuringiensis"
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                                                                                                     /sub_species="kumamotoensis"
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Submitted (15-DEC-1993) Jerald S. Feitelson, Molecular Biology,
Mycogen Corporation, 4980 Carroll Canyon Road, San Diego, CA 92121,
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                                                                                    483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer
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1 (bases 1 to 3507)
Narva,K.E. and Fl.J.
Novel Coleopteran-Active Toxins from Bacillus thuringiensis Unpublished (1994)
2 (bases 1 to 3507)
Peitelson, J.S.
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Bacillus thuringiensis kumamotoensis PS50C(b) CryIII
delta-endotoxin gene, partial cds.
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343 TTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATAGCAGAATATAGCAAGGAATAAA 402 140 AlaLeuhrgGluLeuGluGlyLeuGlnGlyIleMethrgLeutyrGlnThrArgLeuGln 159		259 AsnGlnpheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278 3.1 GCAAAATTAAAAGGCGCTAAACCAATGGATTCCGTAGAAA 822 279 MetThrLeuThrValLeuAspLeuAlaIIeLeuPheProAsnTyrAspProArgArgTyr 298 310 MetThrLeuThrValLeuAspLeuAlaIIeLeuPheProAsnTyrAspProArgArgTyr 298 311 Mid[HisthrLeuValGluAsnGlyAsnAspGlySerGlulleThrHisAsnPheGlybys 396 1108 CATCAAATAAGCATATCGGTACGAGTACCTTTACACAGATGTATGGAACC 1167 397 ThrAspSerlleThrProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerlle 416 1168 AATCAAATTTACAAATTTAGAATTTTAGAATTACGATATTTACAAGCT 1227 417 GluSerLeualaAsglleTyrLeuGlyGlyThrGluAlaAsnAsn 431 1228 TTATCAAATGGTGCAGTACTCTTGATATTTACCAGTATTTACAAGCT 1227 417 GluSer
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5	504 GlyGlyIleValSe	GlyGly1leValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsnAsn	spargaenaen 523
Db 14	486 TCAACTAGCACGTA	ATGTACCTGTATTTTCTTGGACACATCGGAGTGCA	ATCTAACAAAT 1545
δ,	524 ArgLeuGluProAs	ArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsnIl	SlyGlyAsnIle 543
Db 15	546 ACAGTTAAAAGTGC	ACAGTTAAAAGTGGCGAAATCACCCCAAATACCAGGGGGCAAGT	GGCAAGTCTAGCACCATA 1599
ο,	544 GlyP	GlyPheVallleProGlyProThrGlyGlyAsnLeuValLysVal	euValLysVal 558
Db 16	600 GCCAGAAATACTT		TAGTGGCTTTA 1659
δ δ	29	SerAspSerTrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyr	InThrSerTyr 576
Db 16	1660 ACGGACCGCATCGC		AACGATTC 1716
Š	577 ArgileArgLeuAn	ArglleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHi ::	в 596
Db 171	7	GTTACGCT	1737
\$ \$	s 76	erGlySerSerHislleValSerPhePheAspCysSerAsnSer	611
Db 17	1738 rcraatgaaacrac	AGTTTATACGGACTAAA	CTTTAAAATTC 1797
o _y 6	612Se	-SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIl	PheArgTyrile 627
Db 17	1798 AACCAGACATATT	aaccagacatattctaataaaatgaaaatgatttaacatataatgatttcaaatatata	TCAAATATATA 1857
9 %	628 AspvalproGlyIJ	IhrPr	rgThrGlnSer 647
Db 18	1858 GAATATCCAAGAGTCATT	TCATTTCAGTAAATGCTTCTTCAAACATACAGAGGTTATCT	AGAGGTTATCT 1911
و خ	648 PheGlyThrHisAla	lalleAspLysPheGluPheIleProLeu	helleProteu 661
Db 19	1912 ATAGGTATACAAAC	 ataggtatacaaacgaatacaaatttattattttagaccgaatcgaattcatcccagta	rcarccagra 1971
oy oy	662 AgnThrPhePi	ThrPheProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeu	alAsnAspLeu 679
Db 19	972 GATGAGACATATG	CGGA	rearrectre 2031
ò	680 PhelleAsn 682		
DP 20.	 	0.	
RESULT 10 125972 LOCUS DEFINITION ACCESSION VERSION KEYWARDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES BOUICE	125972 Sequence 125972 125972.1 Unknown. Unclassil 1 (bassil Michaels Bacillus	3507 bp DNA linear GI:1605842 GI:1605842 fied. s 1 to 3507) T.E., Narva K.E. and Foncerrada, L. thuringienels toxins active against scarab Location/Qualifiers 1. 3507 1. 3507 /organism="unknown" /mol_type="unassigned DNA"	PAT 07-0CT-1996
Alignment S Pred. No.: Score:		1.45e-60 Length: 3507 942.50 Matches: 249	
Percent Sim	Similarity: 50.	Conservative:	

US-10-782-096-2 (1-682) x I25972 (Gaps: 27 (1-3507)	ପ୍ର	::: :: 988 TCAGAAATAGAAA
		ò	359 PhevalTyrThrA
OY 3 SELIYILYBABILYBABIGI 	SELIYINJAHSHINYAASHAATIYICILMECLEUABDALALEUATGIIEASHSEXASHEE 22 	අු	 1048 ACAGTTTATACAA
23		ò	378 HisThrLeuV
Db 61 TCCAATGATTCTAACAGATA	 TCCAATGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAAATGCGCTACAAAATATG 120	ପ୍ର	
Oy 43 AsnTyrLysGluTrpLeuAsi	MetCysAspSerAsnThrGlnPhelleGlyAspIleSer 62	<i>&</i> :	397 ThrAspSerIleT
Db 121 GATTATAAAGATTATTAAA	GATTATAAAGATTATTTAAAAATGTCTGCGGGAAATGTTAGT 162	යි .	
Oy 63 ThrTyrSerSerProGli	AlaAlaLeuSerValArgAspAlaValLeuThrGlylle 81	<i>हे</i> :	417 GluSer
Db 163 GAATACCCTGGTTCACCTGA		a (
83	AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101	÷ 8	432 IYFILEINESEEG ::: 1270 TATACGTATACAT
223		ò	451 AsnValProGlyS
VY 102 ILETIESERATGLEULIEGI 	IteleserangleulieulylleulipalaulyProasprophedlung	qu	 1330 AATACCAGAAAGA
120		ò	471 Ser
343		q	1378 GATCGGACAAGAG
Qy 140 AlaLeuArgGluLeuGluGl	LeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159	ò	484 GlyAspPheSerH
403		q	1438 GAGTCATATÀC
Oy 160 AlaTrpLeuValAgnLysAgi	AspAspAsnArgArgAlaLeuValThrGlnTyrAla 178	<i>&</i> :	504 GlyGlyIleValS
Db 463 GAGTGGAAAGAAATCCAAAA	GAGTGGAAAGAAATCCAAATGGTTCAAGAGCCTTACGAGATGTTCGAAATCGATTTdAA 522	g (
179		è €	524 ArgheuGluProA: ::::: 1546 ACAGTTAAAAGTG
Db 523 Arccredaracrrrarracc	CAATATATGCCATCTTTTCGAGTGACAAATTTTGAAGTA 582	ìè	544
199	LeuleuleuprovalTyralaGlnalaAsnieuHisleulleleuleuargAspAla 218	3 8	1600 GGCAGAAATACTT
583		È	559 SerAspSerTrpH
219	AspTyrPheGiyAlaGinTrpGinLeuGiyAspAspGiulleArgAspAsnTyrIleArg 238	q	::: 1660 ACGGACCGCATCG
643		ò	577 ArgileArgleuA
Oy 239 LeuGinGiyleulleArgGil	LedcinglyLedileArgGilliYrLySASBHISCYSIIETNrPhelyrAshGInGlyLeu 258	q	1717 CGTATTCGGATTC
50 / 64 C	INITCICACCACICIOIMMETGATATACACTICATITA 762	ò	597 SerGlySerSerH
652	handingturnahang gerkabing dalah garang menging 278 :::This: :: :: GQAAAATTAAAAAGGTTCAAGGTTAAAACAATTAAAAAGGAAAATTAAAAAGGATTAAAAAAAGGATTAAAAAA	qa	1738 TCTAATGAAACTA
279		ò	612Si
823		qa	1798 AACCAGACATATT
299		ò	628 AspValProGlyI
883		qa	1858 GAATATCCAAGAG
Qy 319 GlyValLeuGluSerGlyGly	GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338	ò	648 PheGlyThrHisA
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AAAGCGGCTATTCGTCCACCTCATGTGTTTGATTATAACGGGACTC 1047 ::::::
TATAAGCATATCGGTACGAGTAGTACCTTTACACAGATGTATGGAACC 1167 GCAGTACTCCTTGATATAGTTTACCCTGGT------1269 :::|||::: TTTTTGGAATGCCAGAACCGAGTTTTTTATGGTAAATCAATTGAAT 1329 AAAAAACGTAGCTTCACTTCTGATCGTTATATGAGATATTGGGCTGGT 1107 CAAAGTACTAGCAATTTTGATTTACGAATTACGATATTTACAAGACT 1227 CGTTACGCT------ 1737 GlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIleAsn 450 AspLysileThrGlnIleAspAlaValLysGlyTrpGlyGlyAsnIle 543 HisSerLeuLysValGlnAla-----ProGlnArgGlnThrSerTyr 576 IlePheThrProSerIleAsnProLeulleArgTyrArgThrGlnSer 647 AsnAsnAlaArgArgArgProSerTyrThrThrTrpLeuAsnArgIle 358 ArgThrLeuGlyAsnMetSerAsp---ValArgAsnIleTrpGlyGly 377 ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyLys 396 ThrProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIle 416 -----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsnAsn 431 ------GluLeuProGlyLy8AspLy8ProArgProAsnAla 483 HisArgleuSerTyrIleSerAsnPheAspAlaArgArgSerSerSer 503 SerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsnAsn 523 PheVallleProGlyPro-----ThrGlyGlyAsnLeuValLysVal 558 ArgTyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHis 596 HisIleValSerPhePheAspCysSerAsnSer----- 611 ::: GTCATT-----TCAGTAAATGCTTCTTCAAACATACAGAGGTTATCT

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CC and
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FH Key
FT source
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1 (bases 1 to 3690)
Asano, S., Yamanaka, S. and Takeuchi, K.
Protein having insecticidal activity, DNA encoding the protein, and controlling agent and controlling method of noxious organisms
                                         CAGGTATATICGAGTTCCGTACGCTAGTTTTACACTGCTTGACAAGAATACAGGATCAGGA 1335
                                                                                                       1336 TCAGTTGGAGGTTTTACGTACTCAAAACCACATACAACTATGCAAGTATGTACACAAAAT 1395
                                                                                                                                                                                                                       1510 AGATATGGCAATCTCCCTGTATTTGCTTGGACACATCGGAGTGCGGATGTTACAAATACA 1569
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|GGAAC-TCGCATTTACTC-----TATAAATGTT--AATAAAACCATGAATAAAGGGAAT 1851
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GTTTATTCAGATAAAATTACTCAGATACCAGTTGTAAAAGGCACATACTTTAGTTTCAĠĠŤ
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             SerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnIleAsnAsnValProĠly
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JP 2002045186-A/2.
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OS Bacillus thuringiensis
PN JP 2002045186-A/2
PN JP 2002045186-A/2
PD 12-FRB-2000
PF 03-A016-2000
PI SHINICHIRO ASANO, SATOSHI YAMANAKA, KATSUYOSHI TAKEUCHI PC C12N1/20, A01N63/00, A01N63/02, C07K14/325, C12N1/15, C12N1/19, PC C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20, C12N1/20
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GCTTTAGAGCTTGATTTTGTTGCTAAAATCCCATCTTTTGCAATATCTGGACAGGAAGTA
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2 (bases 1 to 3435)
Asano, S. and Yamamoto, T.
Direct Submission
Submitted (02-ANG-2002) Shin-ichiro Asano, Hokkaido University,
Graduate school of Agriculture, N9W9, Sapporo, Hokkaio 060-8589,
Japan (E-mail:sangakwabs.agr.hokudai.ac.jp, Tel:81-11-706-2423, IleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHisSer GlySerSerHisIleValSerPhePheAspCysSerAsnSerSerGlyArgProSerAsn 2098 TACTCGGATAGCTTAACGGTAGGTGCAGATTCTTTTGCTTCAGGAGAGAAGTTTATGTA ThrieuLeuGluSerAspPheArgTyrIleAspValProGlyIlePheThr---ProSer AsplysPheGluPhelleProLeuAsn---ThrPhe---ProAsnGlnSerLeuGluLys GGTCCGITAGCTTATACTAGTGTCTCTGTAAAATCACCATTATCACAA---AGATATCGT 637 IleAsnProLeuIleArgTyrArgThrGlnSerPhe-----GlyThrHisAlaIle containing -----TrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArg galleriae" Cerf,D. and Yamamoto,T.
A strain of Bacillus thuringiensis subsp. galleriae contain novel cry8 gene highly toxic to Anomala cupres (Coleoptera: Scarabaeidae) Asano, S., Yamashita, C., Iizuka, T., Takeuchi, K., Yamanaka, S. Bacillus thuringiensis serovar galleriae Bacillus thuringiensis serovar galleriae Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus thuringiensis serovar galleriae cry8 gene, AB089299 /organism="Bacillus thuringiensis serovar

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Bacillus thuringiensis
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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                                               ------TrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArg
                                                                                                                                                                              GlySerSerHisIleValSerPhePheAspCysSerAsnSerSerGlyArgProSerAsn
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note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysThraspSerileThrProlleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
                                                                                                                                                         102 IleIleSerArgieuileGlyileLeuTrpAlaGlyProAsp-----ProPheGluAla 119
                                                                                                                                                                                             582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703 CAGATGAAGCTCACCGCGAGTACTCCGACCACTGACGGTGAAGTGGTATGAGACCGGCCTC 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCATGGAGACCAAGGCCCAGCTCACCCGCGAGGTGTACACCGACCCGCTCGGCGCCGTG 942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGTACCCCGGCTCCCCCGAGGTGCTCGTCCGGCCAGGACGCCGCCAAGGCCGCCATC 222
                                                                                                                                                                                                                                                                  Leumet Val Leuval Gluglu Leu Ile Lys Lys Serile Asp Glu Arg Val Arg Glu Asn 139
                                                                                                                                                                                                                                                                                                         AlaLeuArgGlubeuGluGlyLeuGlnGlylleMetArgLeuTyrGlnThrArgLeuGln 159
                                                                                                                                                                                                                                                                                                                                                                                                                                 403 GCCCTCTCCGAGCTGGAGGCCTCGGCAACAACTACCAGCTCTACCTCACCGCCCTGGAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 AlaTrpLeuValAsnLysAsnAspAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 GlyvalLeuGluserGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACGIGICCICCAICGGCICI-----IGGIACGAC---AAGGCCCCAAGCIIC 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 ThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 GAGTGGGAGGAGGAGCCCCCAACGCTCCCGCGCCCTCCGCGACGTGCGCAACGCTTCGAG
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                                                    AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuGlnGlyLeulleArgGluTyrLysAspHisCyslleThrPheTyrAsnGlnGlyLeu
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1276 ---TACATCTTC-----TTCGGCATGCCGGAGGTGGAGTTCTTCATGGTGAACCAGCTC 1326
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                                                                                                                                                  AACAACACCCGCAAGACCCTCAAATAC------AACCCCGTGTCCAAGGACATC 1374
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375 ATGCCTCCACCCGCGACTCCGAGCTCGAGCTCCCCGAGACCTCCGACAGCCCAAC 1434
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                                                                                                                                                                                                                                                                                                                                                                                                            SerGlyGly11eValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn
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                                                                                                                                                                                                  LeuSer------GluLeuProGlyLyBAspLyBProArgProAsn
AsnīyrijeThrSerGlnTyrGlyValSerArgVal ---IlePheAsnThrSerAsnIle
                                                                                               AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle
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